

09/832501

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw mode

Run on: October 27, 2003, 14:53:57 ; Search time 84 Seconds
(without alignments)
1105.417 Million cell updates/sec

Title: US-09-832-501-18

Perfect score: 3103

Sequence: 1 DAHKSEVAHRPKDGEENFK.....TCPAEGKLVAAQAALG- 595

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB	ID	Description
1	3103	100.0	585	10 AAP90388	Mature human serum
2	3103	100.0	585	11 AAR05318	Human serum albumin
3	3103	100.0	585	11 AAR08457	Human serum albumin
4	3103	100.0	585	16 AAR80301	Human serum albumin
5	3103	100.0	585	18 AAO20111	HSA protein sequen
6	3103	100.0	585	21 AAY84873	Amino acid sequenc
7	3103	100.0	585	21 AAY83946	Yeast codon-biased
8	3103	100.0	585	22 ABB79006	Human mature album
9	3103	100.0	585	22 AAE13399	Human albumin (HA)

10	3103	100.0	585	22 AAM52567	Mature human serum
11	3103	100.0	585	22 AAE13129	Human albumin (HA)
12	3103	100.0	585	22 AAE12403	Human albumin (HA)
13	3103	100.0	585	22 AAE08578	Human serum albumin
14	3103	100.0	585	23 ABG71291	Glycosylated prote
15	3103	100.0	585	23 ABG63321	Human serum albumi
16	3103	100.0	585	23 ABJ00986	B lymphocyte stimu
17	3103	100.0	585	23 ABG33847	Human B Lymphocyte
18	3103	100.0	585	23 AAU75220	Mature form of hum
19	3103	100.0	609	21 AAB36542	Recombinant human
20	3103	100.0	609	21 AAB36549	Pre human serum al
21	3103	100.0	609	21 AAY78147	Human serum albumi
22	3103	100.0	609	24 ABUS7252	Human serum albumi
23	3103	100.0	609	24 ABUS7253	Human serum albumi
24	3103	100.0	610	14 AAR38510	Chimeric human ser
25	3103	100.0	616	24 AAE30316	Val8-GLP-1-human s
26	3103	100.0	624	24 AAE30919	Human serum albumi
27	3103	100.0	631	24 AAE30917	Val8-GLP-1-linker-
28	3103	100.0	640	24 AAE30918	Gly8-Gly22-Gly1-C
29	3103	100.0	640	24 AAE30920	Extendin-4-linker-
30	3103	100.0	670	21 AAB36543	Recombinant human
31	3103	100.0	670	21 AAB36550	Recombinant human
32	3103	100.0	783	14 AAR39473	Prepro-HSA-G-CSF c
33	3103	100.0	787	14 AAR39477	G-CSF-(Gly)4-HSA c
34	3103	100.0	853	14 AAR39472	HSA-VWF(470-713) f
35	3099	99.9	585	10 AAP93344	Sequence of mature
36	3099	99.9	585	19 AAM59841	Mature protein of
37	3099	99.9	608	17 AAR96229	Human serum albumi
38	3099	99.9	609	4 AAP30089	Sequence of human
39	3099	99.9	609	17 AAR96232	Human serum albumi
40	3099	99.9	609	17 AAR94572	Cancer metastasis
41	3099	99.9	609	17 AAR88913	Human serum albumi
42	3099	99.9	609	19 AAM48095	Human serum albumi
43	3099	99.9	609	20 AAY06994	Human albumin. HO
44	3099	99.9	609	22 AAB04148	Myosin light chain
45	3099	99.9	609	23 ABG32802	Human serum albumi

ALIGNMENTS

RESULT 1
AAP90388
-D AAP90388 standard; protein: 585 AA.
AC AAP90388;
XX
XX
DT 25-MAR-2003 (updated)
DT 01-NOV-1989 (first entry)
XX
DE Mature human serum albumin polypeptide.
XX
XX Human serum albumin; mature protein; new polypeptides;
KW plasma expanders.
XX
XX Homo sapiens (Human).
XX
XX EP322094-A.
XX
XX 28-JUN-1989.
XX
XX 25-OCT-1988; 88EP-0310000.
XX
XX 30-OCT-1987; 87GB-0025529.
XX
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX
XX Baillance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
XX
XX WPI; 1989-186464/26.
XX
XX N-PSDB; AAN90128.
XX
XX New N-terminal fragments of human serum albumin

P - esp. useful as blood plasma expanders.

XX
PS Disclosure; fig 2; 20pp; English.
XX
CC Mature protein of human serum albumin (see corresp. AAN90128).
CC Used to make new N-terminal fragments which are used as plasma
CC expanders, or as substitutes for HSA or BSA, in tissue culture
CC media.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.5e-255;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGEENFKALVLIAPAOYLQCCPEDHVKLVNEVTEFAKTCVADESAE 60
DB 1 DAHSEVAHRFKDLGEENFKALVLIAPAOYLQCCPEDHVKLVNEVTEFAKTCVADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVRPEV 120
QY 121 DVMCTAFHDNEETPKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 180
DB 121 DVMCTAFHDNEETPKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 180
QY 181 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 181 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
QY 241 VHTCCCHGDLLECCADDRADLAKYICENQDSISSKLKECCCKPLLEKSHCIAEVENDEYPA 300
DB 241 VHTCCCHGDLLECCADDRADLAKYICENQDSISSKLKECCCKPLLEKSHCIAEVENDEYPA 300
QY 301 DPLSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTTLEKC 360
DB 301 DPLSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTTLEKC 360
QY 361 CAADAPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQGLGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADAPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQGLGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALAEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
DB 481 LVNRRPCFSALAEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
QY 541 KEQLKAVMDDFAAFEVKCCCKADDKETCFABEGKKLVAASQAALGL 585
DB 541 KEQLKAVMDDFAAFEVKCCCKADDKETCFABEGKKLVAASQAALGL 585

RESULT 2

AAR05318
ID AAR05318 standard; protein; 585 AA.

XX
AC AAR05318;

DT 08-OCT-1990 (first entry)

XX Human serum albumin gene product.

XX Human serum albumin; HSA-A; yeast; ds.

OS Homo sapiens.

XX JP02117384-A.

PD 01-MAY-1990.
XX
PF 26-OCT-1988; 88JP-0268302.
XX
PR 26-OCT-1988; 88JP-0268302.
XX
PA (TOFU) TOA NENRYO KOGYO KK.
XX
DR KPI; 1990-176228/23.
DR N-PSDB; AAQ04719.
XX
PT Human serum albumin prepn. by yeast host -
PT by culturing transformed plasmid yeast to produce serum, and
PT removing it.
XX
PS Disclosure; Page ?; ?pp; Japanese.
XX
CC Mature HSA-A may be produced using the sequence incorporated into a
CC plasmid vector with suitable controllers, and transferred to a yeast
CC expression system.
XX
SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 11; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.5e-255;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGEENFKALVLIAPAOYLQCCPEDHVKLVNEVTEFAKTCVADESAE 60
DB 1 DAHSEVAHRFKDLGEENFKALVLIAPAOYLQCCPEDHVKLVNEVTEFAKTCVADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLVRPEV 120
QY 121 DVMCTAFHDNEETPKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 180
DB 121 DVMCTAFHDNEETPKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 180
QY 181 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 181 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
QY 241 VHTCCCHGDLLECCADDRADLAKYICENQDSISSKLKECCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCCHGDLLECCADDRADLAKYICENQDSISSKLKECCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DPLSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTTLEKC 360
DB 301 DPLSLAADFVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRKAKTYETTTLEKC 360
QY 361 CAADAPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQGLGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADAPHECYAKVDFEFPKPLVEEPQNLIKQNCSELFQGLGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRLNGKVGSKCKKHPEAKRMPCAEEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALAEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
DB 481 LVNRRPCFSALAEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKKHKPKAT 540
QY 541 KEQLKAVMDDFAAFEVKCCCKADDKETCFABEGKKLVAASQAALGL 585
DB 541 KEQLKAVMDDFAAFEVKCCCKADDKETCFABEGKKLVAASQAALGL 585

RESULT 3

AAR08457
ID AAR08457 standard; protein; 585 AA.

XX
AC AAR08457;

XX 25-MAR-2003 (updated)
 DT 16-APR-1991 (first entry)
 XX Human serum albumin.
 DE HSA: folding; ss.
 KW HSA: folding; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key
 FH Region 123..303
 FT /label= A
 FT Region 1..303
 FT /label= B
 FT Region 123..585
 FT /label= C
 XX JP02227079-A.
 PN 10-SEP-1990.
 PD 25-AUG-1989; 89JP-0217540.
 XX 25-AUG-1989; 89JP-0217540.
 XX (TOFU) TONEN CORP.
 XX WPI; 1990-317325/42.
 DR N-PSDB; AAQ06099.
 XX New human serum albumin fragments - used to bond medicines and for
 PT stable folding of protein(s).
 XX Claim 1; Fig 8; 24pp; Japanese.
 XX Fragments A-C of HSA are expressed as fusion proteins with the
 CC signal peptide of E. coli alkaline phosphatase. The fragments are
 CC selected for their specific properties. The C-terminal truncated
 CC fragment, B, does not bind long-chain fatty acids but does bind to
 CC various medicines at the central region. The N-terminal truncated
 CC fragment, C, has good stability in protein folding. The central
 CC segment, A, has characteristics of both B and C.
 CC See also AAQ06096-Q06098.
 CC (Updated on 25-MAR-2003 to correct PD field.)
 CC (Updated on 25-MAR-2003 to correct PP field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 585 AA;
 SQ
 Query Match 100.0%; Score 3103; DB 11; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHKSEVAHRPKDLGEENFKALVLIAFAQYLQCCPFEDHVKLVNEVTEFAKTCVADSSAE 60
 Db 1 DAHKSEVAHRPKDLGEENFKALVLIAFAQYLQCCPFEDHVKLVNEVTEFAKTCVADSSAE 60
 QY 61 NCKSLHLTFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDNPLRLVRPEV 120
 Db 61 NCKSLHLTFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDNPLRLVRPEV 120
 QY 121 DVMCTAFHDNEETFLUKYLYEYARSHPYFYAPPELLFFAKRYKMAFTECCQAADKAACLLP 180
 Db 121 DVMCTAFHDNEETFLUKYLYEYARSHPYFYAPPELLFFAKRYKMAFTECCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKQRLKASQKQFGERAFKAMAVARLSORFPKAEFAEVSKLVTDLTK 240
 Db 181 KLDELDEGKASSAKQRLKASQKQFGERAFKAMAVARLSORFPKAEFAEVSKLVTDLTK 240
 QY 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLUKCECEKXPPLLEKSHCIAEVENDEMPA 300
 Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLUKCECEKXPPLLEKSHCIAEVENDEMPA 300

QY 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMFLIYAYARRHPDYSVWILLRLAKTYETTLK 360
 Db 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMFLIYAYARRHPDYSVWILLRLAKTYETTLK 360
 QY 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFEQLGEYKFQNALVRYTKKVPQVST 420
 Db 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFEQLGEYKFQNALVRYTKKVPQVST 420
 QY 421 PTLVEVSRNLGVGSKCCCKHPKAPCAEDYLSVYLNQLCVLHEKTPVSDRVTKCCTES 480
 Db 421 PTLVEVSRNLGVGSKCCCKHPKAPCAEDYLSVYLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVGHKPKAT 540
 Db 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVGHKPKAT 540
 QY 541 KEQLKAVMDDFAAVFEKCKCKADDKETCFAEEGKCVAAASQAALGL 585
 Db 541 KEQLKAVMDDFAAVFEKCKCKADDKETCFAEEGKCVAAASQAALGL 585

RESULT 4
 AAR8C301
 ID AAR80301 standard; Protein; 585 AA.
 XX AAR80301;
 AC XX
 DT 25-MAR-2003 (updated)
 DT 17-JAN-1996 (first entry)
 XX Human serum albumin.
 DE Serum albumin; HSA; aspartyl protease-3; Yap3p;
 XX Saccharomycetes cerevisiae.
 KW Homo sapiens.
 OS WO9523857-A1.
 XX 08-SEP-1995.
 XX 01-MAR-1995; 95WO-GB00434.
 XX 03-MAR-1994; 94GB-0004270.
 XX (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX KerryWilliams SM, Gilbert SC;
 XX WPI; 1995-320572/41.
 DR N-PSDB; AAQ98695.
 XX Yeast with reduced levels of aspartyl protease 3 proteolytic
 PT activity - used to secrete human albumin without prodrn. of the 45
 PT kD fragment
 XX Example 1; Page 26-28; 50pp; English.
 XX The cDNA given in AAQ98695, which encodes HSA (AAR80301), was subjected
 CC to site-directed mutagenesis to investigate the role of
 CC endoproteases in the generation of a 45 kDa albumin fragment: obtd.
 CC when the cDNA is expressed in S. cerevisiae. Mutations were: R410A;
 CC L407A, L408V, V409A; and R410A, K413Q, K414Q. The latter set of
 CC mutations, especially, improved stability of HSA to yeast Yap3p
 CC proteolytic cleavage, allowing increased prodrn. of recombinant HSA.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 585 AA;
 SQ

Query Match 100.0%; Score 3103; DB 16; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDGLGENFKALVLIATAFYAOYLQOCPECHVKLVNEVTEPAKTCVADESAAE 60
 Db 1 DAHSEVAHRFKDGLGENFKALVLIATAFYAOYLQOCPECHVKLVNEVTEPAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
 QY 121 DMCTAFHNDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 Db 121 DMCTAFHNDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLOKGERAFKAWAVARLSORPPKAEPAEVSKLVTDLTK 240
 Db 181 KLDELDEGKASSAKORLKCASLOKGERAFKAWAVARLSORPPKAEPAEVSKLVTDLTK 240
 QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCKEKPLEKSHCIAEVENDEMPA 300
 Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCKEKPLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLVEYARRHPDYSVLLLRLAKTYYETTLTK 360
 Db 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLVEYARRHPDYSVLLLRLAKTYYETTLTK 360
 QY 361 CAAADPHECYAKVDFDEPKPLVEEPQNLIKONCELFEQLGGEYKFNALLVRYTKKVPQVST 420
 Db 361 CAAADPHECYAKVDFDEPKPLVEEPQNLIKONCELFEQLGGEYKFNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRLNGKVGSKCKHPKAPKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTES 480
 Db 421 PTLVEVSRLNGKVGSKCKHPKAPKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTUSEKEROIKKOTALVELVGHKPKAT 540
 Db 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTUSEKEROIKKOTALVELVGHKPKAT 540
 QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEKGKLVAAASQAALGL 585
 Db 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEKGKLVAAASQAALGL 585

RESULT 5
 ID AAC20111 standard; Protein; 585 AA.
 AC AAC20111;
 DT 06-AUG-2002 (first entry)
 XX HSA protein sequence related to the growth hormone protein.
 DE Serum albumin-growth hormone fusion protein; growth hormone;
 KW Down's syndrome.
 XX Unidentified.
 OS KR99076789-A.
 PN 15-OCT-1999.
 PD 25-JUN-1998; 98KR-0704914.
 PF 30-DEC-1995; 95GB-0026733.
 PR 19-DEC-1996; 96WO-GB03164.
 PX (DELZ) DELTA BIOTECHNOLOGY LTD.
 PY WPI; 1997-363680/55.
 DR N-PSDB; AAK99568.
 XX Serum albumin-growth hormone fusion protein - useful to treat growth
 PT hormone related diseases, e.g. Down's syndrome

XX Disclosure; Fig 6; 21pp; Korean.
 XX The invention relates to a serum albumin-growth hormone fusion protein -
 CC useful to treat growth hormone related diseases such as Down's syndrome.
 CC This sequence represents a HSA protein related to the serum albumin-
 CC growth hormone protein of the invention.
 XX Sequence 585 AA;
 SQ Query Match 100.0%; Score 3103; DB 18; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDGLGENFKALVLIATAFYAOYLQOCPECHVKLVNEVTEPAKTCVADESAAE 60
 Db 1 DAHSEVAHRFKDGLGENFKALVLIATAFYAOYLQOCPECHVKLVNEVTEPAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
 Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVLRPEV 120
 QY 121 DMCTAFHNDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 Db 121 DMCTAFHNDNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLOKGERAFKAWAVARLSORPPKAEPAEVSKLVTDLTK 240
 Db 181 KLDELDEGKASSAKORLKCASLOKGERAFKAWAVARLSORPPKAEPAEVSKLVTDLTK 240
 QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCKEKPLEKSHCIAEVENDEMPA 300
 Db 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLKECCKEKPLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLVEYARRHPDYSVLLLRLAKTYYETTLTK 360
 Db 301 DLPSLAADFVESKDVCKNYAEAKDVLGMFLVEYARRHPDYSVLLLRLAKTYYETTLTK 360
 QY 361 CAAADPHECYAKVDFDEPKPLVEEPQNLIKONCELFEQLGGEYKFNALLVRYTKKVPQVST 420
 Db 361 CAAADPHECYAKVDFDEPKPLVEEPQNLIKONCELFEQLGGEYKFNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRLNGKVGSKCKHPKAPKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTES 480
 Db 421 PTLVEVSRLNGKVGSKCKHPKAPKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTUSEKEROIKKOTALVELVGHKPKAT 540
 Db 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTUSEKEROIKKOTALVELVGHKPKAT 540
 QY 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEKGKLVAAASQAALGL 585
 Db 541 KEQLKAVMDDDFAAFVEKCKKADDKETCFABEKGKLVAAASQAALGL 585

RESULT 6
 ID AAY84873 standard; protein; 585 AA.
 XX AAY84873;
 AC AAY84873;
 DT 08-AUG-2000 (first entry)
 XX Amino acid sequence of a human albumin protein.
 DE Human; albumin; ischemic state; serum protein; metal ion salt;
 KW peroperative ischemia; ischemia; myocardial infarction;
 KW progressive coronary artery disease.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Modified-site 1

/note= "optionally acetylated, and claimed under claim 56"

PT WO200020840-A1.
XX 13-APR-2000.
XX 01-OCT-1999; 99WO-US22905.
XX 02-OCT-1998; 98US-0102738.
PR 02-OCT-1998; 98US-0165881.
PR 02-OCT-1998; 98US-0165926.
PR 11-JAN-1999; 99US-0115392.
XX (ISCH-) ISCHEMIA TECHNOLOGIES INC.
XX Bar-Or D, Lau E, Winkler JV;
XX WPI; 2000-303843/26.
XX New method for the continuous detection of ischemic states comprises
PT detecting and quantifying the existence of an alteration of the serum
PT protein albumin .
XX Disclosure; Page 97-100; 105pp; English.
XX The present sequence represents human albumin protein. The specification
CC describes a method for the continuous detection of ischemic states. The
CC method comprises detecting and quantifying the existence of an alteration
CC of the serum protein albumin. The method comprises contacting a
CC biological sample containing albumin from the patient with an excess
CC quantity of a metal ion salt, where the metal ion binds to the N-terminus
CC of naturally occurring human albumin, to form a mixture containing bound
CC metal ions and unbound metal ions, and then determining the amount of
CC metal ions bound to the albumin N-terminus. The amount of bound metal
CC ions is correlated to a known value to determine the occurrence or
CC non-occurrence of an ischemic event. The methods are useful for detection
CC of ischemic states. The methods are also useful for distinguishing
CC peripoperative ischemia from ischemia caused by, amongst other things,
CC myocardial infarctions and progressive coronary artery disease.
XX
XX
SQ Sequence 585 AA;
Query Match 100.0%; Score 3103; DB 21; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.5e-255;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHRFKDLGSENFKALVLIAPQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKSEVAHRFKDLGSENFKALVLIAPQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOBERNECEFLQHKDNPMLPRIVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOBERNECEFLQHKDNPMLPRIVRPEV 120
QY 121 DVNCTAFHDNETFLKXLYELARRHPYFYPAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
DB 121 DVNCTAFHDNETFLKXLYELARRHPYFYPAPPELLFFAKRYKAAFTCCQAAADKAACLLP 180
QY 181 KLDELRLDEGKASAKORLJKASLOKQFGERAFKAWAVARLSQRFPAEVAESKLVTDITK 240
DB 181 KLDELRLDEGKASAKORLJKASLOKQFGERAFKAWAVARLSQRFPAEVAESKLVTDITK 240
QY 241 VHTTECHGDLLECAADRADLAKYICENQDISISKLEKCECEKPLLEKSHCIAEVDENMPA 300
DB 241 VHTTECHGDLLECAADRADLAKYICENQDISISKLEKCECEKPLLEKSHCIAEVDENMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHDPDYSVWLLRLAKTYETITLKC 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVLGMLFYEARHDPDYSVWLLRLAKTYETITLKC 360
QY 361 CAAADPHECYAKYVDFEFLVPEEPQNLIKONCELFEQLGEYKFQNALVRYTKKVPQVST 420
DB 361 CAAADPHECYAKYVDFEFLVPEEPQNLIKONCELFEQLGEYKFQNALVRYTKKVPQVST 420

DB 361 CAAADPHECYAKYVDFEFLVPEEPQNLIKONCELFEQLGEYKFQNALVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTES 480
DB 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTES 480
QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTPHAD:CTLSEKERQIKKOTALVELVKKHKPKAT 540
DB 481 LVNRRPCFSALEVDETYVPKEFNAETFTPHAD:CTLSEKERQIKKOTALVELVKKHKPKAT 540
QY 541 KEQLKAVMDDFAAAFVEKCKCKADDDKTCFAEKGKLVAAASQAALGL 585
DB 541 KEQLKAVMDDFAAAFVEKCKCKADDDKTCFAEKGKLVAAASQAALGL 585
RESULT 7
AAV83946
ID AAV83946 standard; Protein; 585 AA.
XX AAV83946;
XX 28-JUL-2000 (first entry)
XX Yeast codon-biased recombinant human serum albumin protein.
XX Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
XX over-lapping oligonucleotide; expression vector.
XX Homo sapiens.
XX Synthetic.
XX CNI2339103-A.
XX 22-DEC-1999.
XX 17-JUN-1998; 98CN-0102506.
XX 17-JUN-1998; 98CN-0102506.
XX (HAIJ-) HAIJI BIOENGINEERING CO LTD.
XX Li S, Lu D;
XX WPI; 2000-351198/31.
XX N-PSDB; AAA10091.
XX Process for preparing recombinant human serum albumin - which comprises
PT yeast biased sex codons
XX Disclosure; Fig 1; 44pp; Chinese.
XX The method relates to a method of recombinantly producing human serum
CC albumin (HSA) in yeast by altering the coding sequence of HSA to
CC comprise a yeast codon bias. The complete HSA gene (AAA10091) was
CC generated as three synthetic fragments (AAA10092-A10094) joined by
CC recombinant DNA technology. Each HSA fragment was synthesised from
CC overlapping oligonucleotide fragments that were extended. This sequence
CC represents the complete sequence of the HSA encoded by the human gene
CC with a yeast codon bias. The invention also covers a recombinant
CC expression vector, yeast host cells carrying the recombinant expression
CC vector and the process for producing human serum albumin in the yeast
CC host cell, especially in secretory mode.
XX
SQ Sequence 585 AA;
Query Match 100.0%; Score 3103; DB 21; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.5e-255;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHRFKDLGSENFKALVLIAPQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKSEVAHRFKDLGSENFKALVLIAPQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60

QY 61 NCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHQDDNPNIPLRVPRPV 120
 DB 61 NCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHQDDNPNIPLRVPRPV 120
 QY 121 DVMTAFHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACJLP 180
 DB 121 DVMTAFHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAAADKAACJLP 180
 QY 181 KLDELDEGKASSAKQRLKASLOKGERAFKAWAVARLSQREPKAEFAEVSKLVTDLT 240
 DB 181 KLDELDEGKASSAKQRLKASLOKGERAFKAWAVARLSQREPKAEFAEVSKLVTDLT 240
 QY 241 VHTCCGDLLECADRADLAKYICENQDSISSKJLKECCCKPJEKSHCIAEVENDEMPA 300
 DB 241 VHTCCGDLLECADRADLAKYICENQDSISSKJLKECCCKPJEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKDVCKNVAEAKDVFLGMFLYKARHPDYSVLLLRJAKTYVETTLK 360
 DB 301 DLPSLAADFVESKDVCKNVAEAKDVFLGMFLYKARHPDYSVLLLRJAKTYVETTLK 360
 QY 361 CAADPHCEYAKVDFEKLVEEPONLIKONCELFEQLGEYKFNALLVRYTKKYPQVST 420
 DB 361 CAADPHCEYAKVDFEKLVEEPONLIKONCELFEQLGEYKFNALLVRYTKKYPQVST 420
 QY 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVVLNQLCVJHEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVVLNQLCVJHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDETVYKPEFNAETFTFHADICTLSEKERQIKKQTALVELVGHKPKAT 540
 DB 481 LVNRRPCFSALEVDETVYKPEFNAETFTFHADICTLSEKERQIKKQTALVELVGHKPKAT 540
 QY 541 KEQLKAVMDFAAFVEKCCCKADKQETCFABEGKGLVAASQAALGL 585
 DB 541 KEQLKAVMDFAAFVEKCCCKADKQETCFABEGKGLVAASQAALGL 585

RESULT 8 ABB79006

ID ABB79006 standard; Protein: 585 AA.

AC ABB79006;

XX 01-AUG-2002 (first entry)

DE Human mature albumin protein SEQ ID NO:18.

XX Human; growth hormone; hGH; albumin; human serum albumin; HSA;
 KW albumin fusion protein; cytosolic; anorectic; immunosuppressive;
 KW antidiabetic; antirheumatic; antiarthritic; psoriatic; cancer;
 KW non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis;
 KW type I diabetes mellitus; rheumatoid arthritis.

OS Homo sapiens.

Key	Location/Qualifiers
FT Domain	1..194
FT	/label= 1
FT Domain	1..105
FT	/label= subdomain
FT Disulfide-bond	53..62
FT Disulfide-bond	75..91
FT Disulfide-bond	90..101
FT Region	106..119
FT	/note= "flexible inter-subdomain linker region"
FT Domain	120..194
FT	/label= subdomain
FT Disulfide-bond	124..169
FT Disulfide-bond	168..177
FT Domain	195..387
FT	/label= 2
FT Domain	195..291
FT	/label= subdomain

FT Disulfide-bond	245..253
FT Disulfide-bond	265..279
FT Disulfide-bond	278..289
FT Region	292..315
FT	/note= "flexible inter-subdomain linker region"
FT Domain	316..387
FT	/label= subdomain
FT Disulfide-bond	316..361
FT Disulfide-bond	360..369
FT Domain	388..585
FT	/label= 3
FT Domain	388..491
FT	/label= subdomain
FT Disulfide-bond	392..438
FT Disulfide-bond	437..448
FT Disulfide-bond	461..477
FT Disulfide-bond	476..487
FT Region	492..511
FT	/note= "flexible inter-subdomain linker region"
FT Domain	512..585
FT	/label= subdomain
FT Disulfide-bond	514..559
FT Disulfide-bond	558..567
XX	WO200179442-A2.
PN	25-OCT-2001.
XX	12-APR-2001; 2001WO-US11850.
PF	12-APR-2000; 2000US-229358P.
PR	25-APR-2000; 2000US-199384P.
PR	21-DEC-2000; 2000US-256931P.
XX	(HUMA-) HUMAN GENOME SCI INC.
XX	Rosen CA, Haseltine WA;
XX	WPI; 2001-611723/70.
DR	N-PSDB; ABB79006.
XX	New albumin fusion proteins, useful for treating diseases and disorders
PT	such as cancer, comprise therapeutic protein fused to albumin -
XX	Claim 1; Fig 11; 413pp; English.
XX	The present invention describes an albumin fusion protein (I) comprising
CC	a therapeutic protein: X and a fragment or variant of albumin
CC	comprising a the fully defined sequence in ABB79006 of 585 amino acids,
CC	(where the fragment or variant has albumin or therapeutic protein: X
CC	activity). (I) can have cytostatic, anorectic, immunosuppressive,
CC	antidiabetic, antirheumatic, antiarthritic and psoriatic activities.
CC	Albumin fusion proteins are stabilised therapeutic proteins e.g.
CC	antibodies to C5, C242 and CD80 useful for treating various diseases
CC	and disorders such as non-Hodgkin's lymphoma, cancer, obesity,
CC	transplant rejection, type I diabetes mellitus, rheumatoid arthritis
CC	and psoriasis. Fusing albumin to therapeutic proteins stabilises the
CC	therapeutic protein, extends the shelf life and retains the in vitro or
CC	in vivo biological activity. It also reduces the need to formulate
CC	protein solutions with large excesses of carrier proteins to prevent
CC	loss of therapeutic proteins due to factors such as binding to the
CC	container. The fusion proteins are easily dispensed with a simple
CC	formulation requiring minimal post storage manipulation. The fusion of
CC	therapeutic proteins to albumin confers stability in aqueous or other
CC	solution. The present sequence represents the mature human albumin (HA)
CC	protein which is used in the exemplification of the present invention.
XX	Sequence 585 AA;
SQ	Query Match 100.0%; Score 3103; DB 22; Length 585;
	Best Local Similarity 100.0%; Pred. No. 9 5e-255;
	Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGSENFKALVLIATAFYLOOCPEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHSEVAHRFKDLGSENFKALVLIATAFYLOOCPEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
QY 121 DVNCTAFHNESTFLKKYLYEYARRHPFYAPDELFFPAKRYKAAFTTECCQAADKAACLLP 180
DB 121 DVNCTAFHNESTFLKKYLYEYARRHPFYAPDELFFPAKRYKAAFTTECCQAADKAACLLP 180
QY 181 KLDLRDEGKASSAKORLKCASLQKGFGERAPKAMAVARLSGRFPKAEFAEVSKLVTDLTK 240
DB 181 KLDLRDEGKASSAKORLKCASLQKGFGERAPKAMAVARLSGRFPKAEFAEVSKLVTDLTK 240
QY 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKLKCECEKPLLEKSHCHIAEVENDEMPA 300
DB 241 VHTTECHGDLLECADDRADLAKYICENQDSISSKLKCECEKPLLEKSHCHIAEVENDEMPA 300
QY 301 DLPSLAADVFESKDVCKNVAEAKOVFLGNFLYEYARRHPDYVSVLLRLAKTYETTLLEK 360
DB 301 DLPSLAADVFESKDVCKNVAEAKOVFLGNFLYEYARRHPDYVSVLLRLAKTYETTLLEK 360
QY 361 CAAADPHECYAKVDFEFKPLVEEPQNLKONCELFQELGEYKFNQALLVRYTKVPQVST 420
DB 361 CAAADPHECYAKVDFEFKPLVEEPQNLKONCELFQELGEYKFNQALLVRYTKVPQVST 420
QY 421 PTLVEVSRNLGVGSKCCKHPKAKMPCAEVLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGVGSKCCKHPKAKMPCAEVLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALVEVDITYVPKFNAEFTTFPHADICTLSEKEROIKKQATLVELVHKPKAT 540
DB 481 LVNRRPCFSALVEVDITYVPKFNAEFTTFPHADICTLSEKEROIKKQATLVELVHKPKAT 540
QY 541 KEQLKAVMDDFAAFEVKCCADDKETCTFAEKGKLVAAASQAALGL 585
DB 541 KEQLKAVMDDFAAFEVKCCADDKETCTFAEKGKLVAAASQAALGL 585

RESULT 9
ID AAE13399
XX AAE13399 standard; Protein; 585 AA.
AC AAE13399;

DT 12-FEB-2002 (first entry)

DE Human albumin (HA) protein.

XX Human; albumin; HA; fusion protein; immune system disorder; syphilis;
KW transplant rejection; blood related disorder; myocardial infarction;
KW hyperproliferative disorder; acute myeloid leukaemia; renal disorder;
KW glomerulonephritis; cardiovascular disorder; arthritmia; rhinitis;
KW respiratory disorder; neurological disease; Alzheimer's disease;
KW endocrine disorder; pheochromocytoma; reproductive system disorder;
KW measles; gastrointestinal disorder; irritable bowel syndrome; HIV;
KW human immunodeficiency virus; wound healing; renal cell carcinoma;
KW melanoma; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Domain 54..61
FT /label= Loop_I
FT /label= Loop_I
FT /label= Loop_II
FT /label= Loop_III
FT /label= Loop_III
FT /label= Loop_IV
FT /label= Loop_IV
FT 247...252

FT Domain /label= Loop_V
FT 266..277
FT /label= Loop_VI
FT 280..288
FT /label= Loop_VII
FT 362..368
FT /label= Loop_VIII
FT 439..447
FT /label= Loop_IX
FT 461..475
FT /label= Loop_X
FT 478..486
FT /label= Loop_XI
FT 560..566
FT /label= Loop_XII

XX WO200179258-A1.

XX 25-OCT-2001.

XX 12-APR-2001; 2001WO-US12008.

XX 12-APR-2000; 2000US-229358P.

XX 25-APR-2000; 2000US-199384P.

XX 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (PRIN-) PRINCIPAL PHARM CORP.

XX Rosen CA, Sadeghi H, Prior CP, Turner AJ;

XX WPI; 2001-602931/68.

XX N-PSDB; AAD22287.

XX Albumin fusion proteins comprising a therapeutic protein and albumin,
XX useful in the treating metastatic renal cell carcinoma, metastatic
XX melanoma, malignant melanoma, renal cell carcinoma, HIV (human
XX immunodeficiency virus) or infection -
XX
XX Claim 1; Fig 9; 325pp; English.

XX The invention relates to albumin fusion proteins comprising therapeutic
XX protein and human albumin (HA). The albumin fusion proteins are useful
XX in the treatment, prevention, diagnosis, and/or detection of diseases,
XX disorders such as immune system disorders (transplant rejection); blood
XX related disorders (myocardial infarction); hyperproliferative disorders
XX (childhood acute myeloid leukaemia); renal disorder (glomerulonephritis);
XX cardiovascular disorders (arrhythmias); respiratory disorders
XX (non-allergic rhinitis); neurological diseases (Alzheimer's disease);
XX endocrine disorders (pheochromocytoma); reproductive system disorders
XX (syphilis); infectious diseases (measles); gastrointestinal disorders
XX (irritable bowel syndrome) and wound healing. The albumin fusion
XX proteins are also used in the treatment of metastatic renal cell
XX carcinoma, metastatic melanoma, malignant melanoma and HIV (human
XX immunodeficiency virus) infection. Nucleic acid encoding albumin fusion
XX protein is useful in gene therapy. The present sequence is human
XX albumin (HA) protein.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.5e-255;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLGSENFKALVLIATAFYLOOCPEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHSEVAHRFKDLGSENFKALVLIATAFYLOOCPEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
QY 121 DVNCTAFHNESTFLKKYLYEYARRHPFYAPDELFFPAKRYKAAFTTECCQAADKAACLLP 180

Db 121 DVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAAKAAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLOKGEGERAFKAWAVARLSORPPKAEFAEVSUKLVTDLT 240
 Db 181 KLDELDEGKASSAKORLKCASLOKGEGERAFKAWAVARLSORPPKAEFAEVSUKLVTDLT 240
 QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLECCCKPPLLEKSHCIAEVENDEMPA 300
 Db 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLECCCKPPLLEKSHCIAEVENDEMPA 300
 QY 301 DPLSLAADFVESKDVCKNYAEAKDVFGLMFLYEYARRHPDYISVVLRLRLAKTYETTTLEK 360
 Db 301 DPLSLAADFVESKDVCKNYAEAKDVFGLMFLYEYARRHPDYISVVLRLRLAKTYETTTLEK 360
 QY 361 CAADDPHECYAKVDFEFPKPLVEEPONLIKONCELFQOLGEYKFORALVRYTKVPQVST 420
 Db 361 CAADDPHECYAKVDFEFPKPLVEEPONLIKONCELFQOLGEYKFORALVRYTKVPQVST 420
 QY 421 PTLVEVSRLNGKVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 Db 421 PTLVEVSRLNGKVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDVETVYVPKFEFNAETTFTHADICTLSEKERQIKKQATALVELVGHKPKAT 540
 Db 481 LVNRRPCFSALEVDVETVYVPKFEFNAETTFTHADICTLSEKERQIKKQATALVELVGHKPKAT 540
 QY 541 KEOLKAVMDDFAAFEVKCKKADDDKTCFAEBGKLVAAASQAALGL 585
 Db 541 KEOLKAVMDDFAAFEVKCKKADDDKTCFAEBGKLVAAASQAALGL 585

RESULT 10

AAW52567
 ID AAW52567 standard; Protein; 585 AA.

XX AC AAW52567;

XX DT 05-FEB-2002 (first entry)

XX DE Mature human serum albumin.

XX KW Human; serum albumin; HA; antiinflammatory; immunosuppressive; cardiac;
 KW neotropic; neuroprotective; gene therapy; immune disorder; wound healing;
 KW hyperproliferative disorder; renal disorder; cardiovascular disorder;
 KW respiratory disorder; neurological disease; endocrine disorder;
 KW reproductive system disorder; infectious disease;
 KW gastrointestinal disorder.

XX OS Homo sapiens.

XX PN W0200179444-A2.

XX PD 25-OCT-2001.

XX PF 12-APR-2001; 2001WO-US12013.

XX PR 12-APR-2000; 2000US-229358P.

XX PR 25-APR-2000; 2000US-199384P.

XX PR 21-DEC-2000; 2000US-256931P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Haseltine WA;

XX DR WPI; 2001-616755/71.

XX DR N-PSDB; ABA03057.

XX PT Albumin fusion proteins comprising a therapeutic protein and albumin,
 PT useful in the treating immune system disorders (e.g. transplant
 PT rejection), blood related disorders (e.g. myocardial infarction) and
 PT hyperproliferative disorders -

XX

PS Claim 1; Fig 15; 606pp; English.
 XX The present invention relates to albumin fusion proteins, which comprise
 CC a therapeutic protein and albumin. The present sequence is the protein
 CC sequence for mature human serum albumin (HA), which was used to generate
 CC the fusion proteins of the present invention. The albumin fusion proteins
 CC are useful in the treatment, prevention, diagnosis, and/or detection of
 CC diseases/disorders such as immune system disorders (e.g. transplant
 CC rejection), blood related disorders (e.g. myocardial infarction),
 CC hyperproliferative disorders (e.g. childhood acute myeloid leukemia),
 CC renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g.
 CC arrhythmias), respiratory disorders (e.g. non-allergic rhinitis),
 CC neurological diseases (e.g. Alzheimer's disease), endocrine disorders
 CC (e.g. pheochromocytoma), reproductive system disorders (e.g. syphilis),
 CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
 CC irritable bowel syndrome) and wound healing.

XX Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKOLGEENFKALVLIAPAYLOQCPEPDHVKLVNEVTEFAKTCVADESAE 60

Db 1 DAHKSEVAHRFKOLGEENFKALVLIAPAYLOQCPEPDHVKLVNEVTEFAKTCVADESAE 60

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKCEPERNECFLOHKDDNPNLRLVRPEV 120

Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKCEPERNECFLOHKDDNPNLRLVRPEV 120

QY 121 DVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAAKAAACLLP 180

Db 121 DVNCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAAKAAACLLP 180

QY 181 KLDELDEGKASSAKORLKCASLOKGEGERAFKAWAVARLSORPPKAEFAEVSUKLVTDLT 240

Db 181 KLDELDEGKASSAKORLKCASLOKGEGERAFKAWAVARLSORPPKAEFAEVSUKLVTDLT 240

QY 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLECCCKPPLLEKSHCIAEVENDEMPA 300

Db 241 VHTTECHGDLLECCADRADLAKYICENQDSISSKLECCCKPPLLEKSHCIAEVENDEMPA 300

QY 301 DPLSLAADFVESKDVCKNYAEAKDVFGLMFLYEYARRHPDYISVVLRLRLAKTYETTTLEK 360

Db 301 DPLSLAADFVESKDVCKNYAEAKDVFGLMFLYEYARRHPDYISVVLRLRLAKTYETTTLEK 360

QY 361 CAADDPHECYAKVDFEFPKPLVEEPONLIKONCELFQOLGEYKFORALVRYTKVPQVST 420

Db 361 CAADDPHECYAKVDFEFPKPLVEEPONLIKONCELFQOLGEYKFORALVRYTKVPQVST 420

QY 421 PTLVEVSRLNGKVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

Db 421 PTLVEVSRLNGKVGSKCKHPKAPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

QY 481 LVNRRPCFSALEVDVETVYVPKFEFNAETTFTHADICTLSEKERQIKKQATALVELVGHKPKAT 540

Db 481 LVNRRPCFSALEVDVETVYVPKFEFNAETTFTHADICTLSEKERQIKKQATALVELVGHKPKAT 540

QY 541 KEOLKAVMDDFAAFEVKCKKADDDKTCFAEBGKLVAAASQAALGL 585

Db 541 KEOLKAVMDDFAAFEVKCKKADDDKTCFAEBGKLVAAASQAALGL 585

RESULT 11

AAE13129
 ID AAE13129 standard; Protein; 585 AA.

XX AC AAE13129;

XX DT 28-JAN-2002 (first entry)

XX DE Human albumin (HA).

XX Human; albumin; HA; fusion protein; therapeutic protein; vulnereary;
 KW immune system disorder; transplant rejection; blood related disorder;
 KW myocardial infarction; hyperproliferative disorder; glomerulonephritis;
 KW childhood acute myeloid leukemia; cardiovascular disorder; arrhythmia;
 KW respiratory disorder; gene therapy; non-allergic rhinitis; noctropic;
 KW neurological disease; Alzheimer's disease; reproductive system disorder;
 KW endocrine disorder; pheochromocytoma; infectious disease; antiarthritic;
 KW measles; gastrointestinal disorder; irritable bowel syndrome; syphilis;
 KW wound healing; antiinflammatory; immunosuppressive; neuroprotective;
 KW cardiant; cytostatic; antileukaemic; antirheumatic; antimicrobial;
 KW renal disorder.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Domain 54..61 /label= Loop_I
 FT Domain 76..89 /label= Loop_II
 FT Domain 92..100 /label= Loop_III
 FT Domain 170..176 /label= Loop_IV
 FT Domain 247..252 /label= Loop_V
 FT Domain 266..277 /label= Loop_VI
 FT Domain 280..288 /label= Loop_VII
 FT Domain 362..368 /label= Loop_VIII
 FT Domain 439..447 /label= Loop_IX
 FT Domain 461..475 /label= Loop_X
 FT Domain 478..486 /label= Loop_XI
 FT Domain 560..566 /label= Loop_XII
 FT
 PN WO200179443-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US11924.
 XX
 PR 12-APR-2000; 2000US-229358P.
 PR 25-APR-2000; 2000US-199384P.
 PR 21-DEC-2000; 2000US-256931P.
 XX
 PA (HUYA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CR, Haseltine WA;
 PI
 DR WPI; 2001-616754/71.
 DR N-PSDB; AAD21638.
 XX
 PT Albumin fusion proteins comprising a therapeutic protein and albumin,
 PT useful in the treating immune system disorders (e.g. transplant
 PT rejection), blood related disorders (e.g. myocardial infarction) and
 PT hyperproliferative disorders -
 XX
 PS Claim 1; Fig 9; 380pp; English.
 XX
 CC The invention relates to albumin fusion proteins comprising therapeutic
 CC protein and human albumin (HA). Therapeutic protein fused to albumin
 CC have an extended shelf-life. The albumin fusion proteins are useful in
 CC the treatment, prevention, diagnosis and/or detection of diseases,
 CC disorders such as immune system disorders (e.g. transplant rejection),
 CC blood related disorders (e.g. myocardial infarction), hyperproliferative
 CC disorders (e.g. childhood acute myeloid leukaemia), renal disorders
 CC (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias),

CC respiratory disorders (e.g. non-allergic rhinitis), neurological
 CC diseases (e.g. Alzheimer's disease), endocrine disorders (e.g.
 CC pheochromocytoma), reproductive system disorders (e.g. syphilis),
 CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
 CC irritable bowel syndrome) and wound healing. Nucleic acids encoding
 CC albumin fusion protein is used in gene therapy. The present sequence
 CC is human albumin (HA) protein.
 XX
 SQ Sequence 585 AA;
 Query Match 100.0%; Score 3103; DS 22; Length 585;
 Best Local Similarity 100.0%; Pred. No. 9.5e-255;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHKEVAHRFKDGLGEENFKALVLI AFAQYLOQC PFEDHVKVNEVTEFAKTCVADESAAE 60
 DB 1 DAHKEVAHRFKDGLGEENFKALVLI AFAQYLOQC PFEDHVKVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDNPRLVRREV 120
 DB 61 NCDKSLHTFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDNPRLVRREV 120
 QY 121 DVNCTAFHDNEETFLKKYLYEIARRHPYFAPPELLFFAKRYKAAFTCCOAAADKAACLLP 180
 DB 121 DVNCTAFHDNEETFLKKYLYEIARRHPYFAPPELLFFAKRYKAAFTCCOAAADKAACLLP 180
 QY 181 KJDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSQRFPAKFAEVSCLVDTLTK 240
 DB 181 KJDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSQRFPAKFAEVSCLVDTLTK 240
 QY 241 VHTECHGDLLECADDRADLAKYICENODSISSKLECECEKELLESKHCIAEVNDENMPA 300
 DB 241 VHTECHGDLLECADDRADLAKYICENODSISSKLECECEKELLESKHCIAEVNDENMPA 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRJAKTYETTLKCC 360
 DB 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRJAKTYETTLKCC 360
 QY 361 CAAADPHECYAKVDFEPKPLVEEPQNLIKONCELFEQGEYKFNALLVRYTKVPQVST 420
 DB 361 CAAADPHECYAKVDFEPKPLVEEPQNLIKONCELFEQGEYKFNALLVRYTKVPQVST 420
 QY 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDVLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRNLGKVGSKCKKHPKAPCAEDVLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPFSALAEVDETYVPKFENAEITTFHADICTLSEKERQIKQTALVELVHKPKAT 540
 DB 481 LVNRRPFSALAEVDETYVPKFENAEITTFHADICTLSEKERQIKQTALVELVHKPKAT 540
 QY 541 KEQLKAVMDPFAAFVEKCKCKADDKETCFABEGKLVVAASQAALGL 585
 DB 541 KEQLKAVMDPFAAFVEKCKCKADDKETCFABEGKLVVAASQAALGL 585
 RESULT 12
 AAEL2403
 ID AAEL2403 standard; Protein; 585 AA.
 XX
 AC AAEL2403;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human albumin (HA).
 XX
 KW Human; albumin; HA; immune system disorder; transplant rejection;
 KW blood related disorder; myocardial infarction; glomerulonephritis;
 KW hyperproliferative disorder; childhood acute myeloid leukaemia;
 KW renal cell carcinoma; cardiovascular disorder; vulnereary; melanoma;
 KW arrhythmia; respiratory disorder; non-allergic rhinitis; antileukaemic;
 KW neurological disease; Alzheimer's disease; endocrine disorder; measles;
 KW pheochromocytoma; reproductive system disorder; neuroprotective; syphilis;
 KW infectious disease; gastrointestinal disorder; wound healing; noctropic;

KW irritable bowel syndrome; HIV; human immunodeficiency virus infection;
 KW cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant;
 KW antirheumatic; antirheumatic; renal disorder; antimicrobial.

OS Homo sapiens.

XX Key Location/Qualifiers
 PH Domain 54..61
 FT /label= Loop_I
 FT Domain 76..89
 FT /label= Loop_II
 FT Domain 92..100
 FT /label= Loop_III
 FT Domain 170..176
 FT /label= Loop_IV
 FT Domain 247..252
 FT /label= Loop_V
 FT Domain 266..277
 FT /label= Loop_VI
 FT Domain 280..288
 FT /label= Loop_VII
 FT Domain 362..368
 FT /label= Loop_VIII
 FT Domain 439..447
 FT /label= Loop_IX
 FT Domain 461..475
 FT /label= Loop_X
 FT Domain 478..486
 FT /label= Loop_XI
 FT Domain 560..566
 FT /label= Loop_XII

WO200179480-A1.

25-OCT-2001.

12-APR-2001; 2001WO-US11991.

12-APR-2000; 2000US-229358P.

25-APR-2000; 2000US-199384P.

21-DEC-2000; 2000US-256931P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Haseltine WA;

WPI; 2001-616756/71.

N-PSDB; AAD20005.

Albumin fusion proteins comprising a therapeutic protein and albumin,
 useful in the treating metastatic renal cell carcinoma, metastatic
 melanoma, malignant melanoma, renal cell carcinoma, HIV (human
 immunodeficiency virus) or infection -

Claim 1; Fig 9; 394pp; English.

The invention relates to human albumin (HA) fusion proteins and their
 corresponding nucleic acid sequences. Therapeutic proteins fused to
 albumin or its fragments have an extended shelf-life. The albumin
 fusion proteins are useful in the treatment, prevention, diagnosis,
 and/or detection of diseases, disorders such as immune system
 disorders (e.g. transplant rejection), blood related disorders (e.g.
 myocardial infarction), hyperproliferative disorders (e.g. childhood
 acute myeloid leukaemia, metastatic renal cell carcinoma, metastatic
 melanoma, malignant melanoma, renal cell carcinoma), renal disorders
 (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias),
 respiratory disorders (e.g. non-allergic rhinitis), neurological
 diseases (e.g. Alzheimer's disease), endocrine disorders (e.g.
 pheochromocytoma), reproductive system disorders (e.g. syphilis),
 infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
 irritable bowel syndrome), HIV (human immunodeficiency virus) infection
 and wound healing. Nucleic acids encoding albumin fusion protein is
 used in gene therapy. The present sequence is human albumin.

XX	Sequence	585 AA;
XX	Query Match	100.0%; Score 3103; DB 22; Length 585;
XX	Best Local Similarity	100.0%; Pred. No. 9.5e-255;
XX	Matches	585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DAKSEVAHRPKOLGEENFKALVLI	FAQYLOQCPEDHVKLVNEVTERAKT	CVADSEAE	60
DB	1	DAKSEVAHRPKOLGEENFKALVLI	FAQYLOQCPEDHVKLVNEVTERAKT	CVADSEAE	60
QY	61	NCDSLHTLFGDKLCTVATLRETY	GEMADCCAKOEPERNECFLOHKD	NDNPNLPRVPEV	120
DB	61	NCDSLHTLFGDKLCTVATLRETY	GEMADCCAKOEPERNECFLOHKD	NDNPNLPRVPEV	120
QY	121	DVMCTAFHDNEETFLKYLVEIAR	RRHPFYFAPELLFFAKRYKAAFT	ECCEAAKAAACLLP	180
DB	121	DVMCTAFHDNEETFLKYLVEIAR	RRHPFYFAPELLFFAKRYKAAFT	ECCEAAKAAACLLP	180
QY	181	KLDELDEGKASSAKORLKCASLQ	KFGERAFKAWAVARLSORFPKAE	FAEVSKLVTDLTK	240
DB	181	KLDELDEGKASSAKORLKCASLQ	KFGERAFKAWAVARLSORFPKAE	FAEVSKLVTDLTK	240
QY	241	VHTECCHGDLLECADRADLAKYI	CENQDSISSKLEKCEKPLLEKSH	CHCIAEVENDEMPA	300
DB	241	VHTECCHGDLLECADRADLAKYI	CENQDSISSKLEKCEKPLLEKSH	CHCIAEVENDEMPA	300
QY	301	DLPSLAADFVESKDVCKNYAEAK	DVFLGMFLYEYARRHPDYSVLL	LLRLAKTYTTLEKC	360
DB	301	DLPSLAADFVESKDVCKNYAEAK	DVFLGMFLYEYARRHPDYSVLL	LLRLAKTYTTLEKC	360
QY	361	CAAADPHECYAKVFDEFKPLVEE	PQNLIKONCELFEOQGEYKFONAL	LVRVTKVPQVST	420
DB	361	CAAADPHECYAKVFDEFKPLVEE	PQNLIKONCELFEOQGEYKFONAL	LVRVTKVPQVST	420
QY	421	PTLVEVSRNLGKVGSKCKGHPK	AKMPCAEYLSVWLNQLCVLHEKT	PVSDRVTKCCTES	480
DB	421	PTLVEVSRNLGKVGSKCKGHPK	AKMPCAEYLSVWLNQLCVLHEKT	PVSDRVTKCCTES	480
QY	481	LVNRRPCPSALEVDETYPKFEF	NAETTFHADICTLSEKERQIKKOT	ALVELVGHKPKAT	540
DB	481	LVNRRPCPSALEVDETYPKFEF	NAETTFHADICTLSEKERQIKKOT	ALVELVGHKPKAT	540
QY	541	KEQLKAVNDDFAAFVEKCKKAD	DKETCFABEGKKLVAASQAALGL	585	
DB	541	KEQLKAVNDDFAAFVEKCKKAD	DKETCFABEGKKLVAASQAALGL	585	

RESULT 13

AAE08578

ID AAE08578 standard; Protein; 585 AA.

XX

AC AAE08578;

XX

DT 19-NOV-2001 (first entry)

XX

DE Human serum albumin (HSA).

XX

KW Human; albumin; cancer; cell proliferation; drug screening; biopsy.

XX

OS Homo sapiens.

XX

PN US6274305-B1.

XX

PD 14-AUG-2001.

XX

PF 19-DEC-1996; 96US-0769746.

XX

PR 19-DEC-1996; 96US-0769746.

XX

PA (TUFT) UNIV TUFTS.

XX

PI Somnenschein C, Soto AM;

```
XX DR WPI; 2001-540371/60.
XX DR N-PSDB; AAD11488.
XX PT Measuring human cell proliferation, useful in drug screening to
XX PT determine the potential for inhibiting cancer cell proliferation and
XX PT for evaluating biopsied tumors, comprises employing albumin-derived
XX PT peptide -
XX PS
XX PS Claim 1; Fig 1; 20pp; English.
XX CC The invention related to a method for testing cancer cells. The method is
XX CC useful for measuring human cancer cell proliferation, particularly for
XX CC determining the potential for inhibiting cancer cell's proliferation using
XX CC albumin-derived peptides. The invention is also useful for drug screening
XX CC assays, as well as for evaluating biopsied tumors. The present sequence
XX CC is human serum albumin (HSA) related to the invention.
XX SQ Sequence 585 AA;
XX
XX Query Match 100.0%; Score 3103; DB 22; Length 585;
XX Best Local Similarity 100.0%; Pred. No. 9.5e-255;
XX Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DAHSEVAHRFKDGLGEENFKALVLIIFAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 60
DB 1 DAHSEVAHRFKDGLGEENFKALVLIIFAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFQHKDDNPRLVRPEV 120
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPFYFVAPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKKYLVEIARRHPFYFVAPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 181 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCEKPLLEKSHCIAEVENDENMPA 300
DB 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCEKPLLEKSHCIAEVENDENMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLEYARRHPDYSVVLRLRAKTYETTLEK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLEYARRHPDYSVVLRLRAKTYETTLEK 360
QY 361 CAAADPHECYAKVDFEKPPLVEBPQNLIKONCELFEQLGVEYKFNALLVRYTKKVPQVST 420
DB 361 CAAADPHECYAKVDFEKPPLVEBPQNLIKONCELFEQLGVEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRLNGLKVGSKCKKHPKAEKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRLNGLKVGSKCKKHPKAEKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDVETVYPKEFNAETFTFHADICTLSEKERQIKKQTAJVELVKKHPKAT 540
DB 481 LVNRRPCFSALEVDVETVYPKEFNAETFTFHADICTLSEKERQIKKQTAJVELVKKHPKAT 540
QY 541 KEQLKAVMDQFAFVEKCCCKADDKETCFABEGKKLVAASQAALGL 585
DB 541 KEQLKAVMDQFAFVEKCCCKADDKETCFABEGKKLVAASQAALGL 585
XX
XX RESULT 14
XX ID ABG71291
XX AC ABG71291;
XX DT 08-JAN-2003 (first entry)
XX
```

```
DE Glycosylated protein determination associated protein.
XX Standard substance; accuracy control substance; glycosylated protein;
KW glycosylated albumin; fructosamine; diabetes; antidiabetic.
CS Unidentified.
XX JP2002243731-A.
XX 28-AUG-2002.
XX 21-FEB-2001; 2001JP-0045085.
XX 21-FEB-2001; 2001JP-0045085.
XX (KOKU-) KOKUSAI SHIYAKU KK.
XX (YOSH) YOSHITOMI PHARM IND KK.
XX WPI; 2002-744850/81.
XX A standard substance for determination of glycosylated protein
PT including glycosylated albumin and fructosamine, used in diagnosis of
PT diabetes.
XX Disclosure; Page 4; 6pp; Japanese.
XX The present invention relates to a new standard and accuracy control
XX substance for determination of glycosylated protein. The invention is
XX useful for determination of glycosylated protein in the diagnosis of
XX diabetes. Glycosylated albumin and fructosamine provide favorable
XX dilution linearity. The present amino acid sequence represents the
XX glycosylated protein determination associated protein as described in
XX the invention.
XX SQ Sequence 585 AA;
XX
XX Query Match 100.0%; Score 3103; DB 23; Length 585;
XX Best Local Similarity 100.0%; Pred. No. 9.5e-255;
XX Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DAHSEVAHRFKDGLGEENFKALVLIIFAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 60
DB 1 DAHSEVAHRFKDGLGEENFKALVLIIFAQYLOQCPFEDHVKLVNEVTEFAKTCVADESAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVRPEV 120
QY 121 DVMTAFHDNEETFLKKYLVEIARRHPFYFVAPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVMTAFHDNEETFLKKYLVEIARRHPFYFVAPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 181 KLDELDEGRKASSAKQRLKASLQKFGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
QY 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCEKPLLEKSHCIAEVENDENMPA 300
DB 241 VHTCCCHGDLLECADRADLAKYICENQDSISSKLECCCEKPLLEKSHCIAEVENDENMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLEYARRHPDYSVVLRLRAKTYETTLEK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLEYARRHPDYSVVLRLRAKTYETTLEK 360
QY 361 CAAADPHECYAKVDFEKPPLVEBPQNLIKONCELFEQLGVEYKFNALLVRYTKKVPQVST 420
DB 361 CAAADPHECYAKVDFEKPPLVEBPQNLIKONCELFEQLGVEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRLNGLKVGSKCKKHPKAEKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRLNGLKVGSKCKKHPKAEKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDVETVYPKEFNAETFTFHADICTLSEKERQIKKQTAJVELVKKHPKAT 540
```

Db 481 LVNRRPCFSALEVDETVVPKEFNAETFTFHADICTLSEKERQ:KKQTALVELVGHKPKAT 540
Qy 541 KEQLKAVMDDFAAATVEKCCXADDKETCFABEGKLVAAASQAALGL 585
Db 541 KEQLKAVMDDFAAATVEKCCXADDKETCFABEGKLVAAASQAALGL 585

RESULT 15
ABG63321
ID ABG63321 standard; protein; 585 AA.
AC ABG63321;
DT 27-AUG-2002 (first entry)
XX Human serum albumin (HSA) protein.
DE
XX
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytosstatic; antifertility; antiinflammatory; antiulcer;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.
XX
OS Homo sapiens.
XX
XX WO200177137-A1.
XX
XX 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US11988.
XX
XX 12-APR-2000; 2000US-229358P.
XX 25-APR-2000; 2000US-199384P.
XX 21-DEC-2000; 2000US-256931P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Haseltine WA;
XX
XX WPI; 2002-010886/01.
XX DR N-PSDB; ABK93280.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an:
XX albumin fused to a therapeutic protein -
XX
XX Claim 1; Fig 15; 2102pp; English.
XX
XX The present invention relates to albumin fusion proteins comprising a
XX therapeutic protein X and human albumin (HA, also known as human serum:
XX albumin, HSA). The proteins are useful for treating a disease or
XX disorder that may be modulated by therapeutic protein X. The albumin
XX extends the shelf-life of protein X, and may increase its biological
XX in vitro/in vivo activity. The protein is useful for treating and
XX diagnosing disorders such as cancer, reproductive disorders, digestive
XX disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
XX (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
XX (e.g. diabetes), haematopoietic disorders, neural disorders
XX (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
XX encephalomyelitis, meningitis, schizophrenia), and connective disorders
XX (e.g. osteoporosis, arthritis). The present sequence represents HSA
XX (HA) protein.
XX
SQ Sequence 585 AA;

Query Match 100.0%; Score 3103; DB 23; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.5e-255;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy. . . 1 DAHKSEVAHREKDLGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60

Db 1 DAHKSEVAHREKDLGEENFKALVLIAPAYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDGNPKLPVLVPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDGNPKLPVLVPEV 120
Qy 121 DVMCTAFHDNEETFLKYYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQQAADKAACILP 180
Db 121 DVMCTAFHDNEETFLKYYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQQAADKAACILP 180
Qy 181 KLDELDEGKASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAKFAEVSKLVTDLTK 240
Db 181 KLDELDEGKASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAKFAEVSKLVTDLTK 240
Qy 241 VHTCCHGDLLECADDDRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDMPA 300
Db 241 VHTCCHGDLLECADDDRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDMPA 300
Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLYEYARRHPDYSVVLLLRLAITYETTTLEKC 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFGLMFLYEYARRHPDYSVVLLLRLAITYETTTLEKC 360
Qy 361 CAAADPHECYAKVPDEFKPLVVEEPONLIKONCELLFEQLGEYKFONALLVRYTKVPQVST 420
Db 361 CAAADPHECYAKVPDEFKPLVVEEPONLIKONCELLFEQLGEYKFONALLVRYTKVPQVST 420
Qy 421 PTLVEVSRNLGKVGSKCKCKHPEAKEMPCAEDYLSVLNQLCVLHEKTPVSORVTKCCTES 480
Db 421 PTLVEVSRNLGKVGSKCKCKHPEAKEMPCAEDYLSVLNQLCVLHEKTPVSORVTKCCTES 480
Qy 481 LVNRRPCFSALEVDETVVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVGHKPKAT 540
Db 481 LVNRRPCFSALEVDETVVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVGHKPKAT 540
Qy 541 KEQLKAVMDDFAAATVEKCCXADDKETCFABEGKLVAAASQAALGL 585
Db 541 KEQLKAVMDDFAAATVEKCCXADDKETCFABEGKLVAAASQAALGL 585

Search completed: October 27, 2003, 15:04:45
Job time : 89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2003, 15:03:17 ; Search time 29 Seconds
(without alignments)
853.512 Million cell updates/sec

Title: US-09-832-501-18

Perfect score: 3103
Sequence: 1 DAHSEVAHRFKDLGEENFK.....TCFAEEGKKVAASQAALGQ 585

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/protdata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/protdata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/protdata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/protdata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/protdata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/protdata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3103	100.0	585	1	US-08-153-799-14
2	3103	100.0	585	2	US-08-702-572-2
3	3103	100.0	585	3	US-08-769-746-2
4	3103	100.0	610	2	US-08-797-689-2
5	3103	100.0	783	1	US-08-256-938-2
6	3103	100.0	787	1	US-08-256-938-4
7	3103	100.0	787	2	US-08-797-689-16
8	3099	99.9	609	1	US-08-222-619-3
9	3099	99.9	609	1	US-08-433-037-4
10	3099	99.9	609	4	US-08-897-956A-2
11	3099	99.9	609	5	PCT-US95-04075-3
12	3095	99.7	978	4	US-08-897-956A-3
13	3093	99.7	585	2	US-08-448-196A-3
14	3093	99.7	585	2	US-08-984-176-1
15	2458.5	79.2	583	1	US-08-448-196A-5
16	2450.5	79.0	583	1	US-08-448-196A-6
17	2432.5	78.4	583	1	US-08-448-196A-7
18	2426	78.2	584	1	US-08-448-196A-7
19	2389	77.0	582	1	US-08-134-638-1
20	1249.5	40.3	609	1	US-08-222-619-4
21	1249.5	40.3	609	5	PCT-US95-04075-4
22	1206.5	38.9	590	2	US-08-377-309-2
23	1206.5	38.9	590	3	US-09-186-723-2
24	1206.5	38.9	590	4	US-08-505-012-5
25	1206.5	38.9	590	4	US-09-186-949A-3
26	1206.5	38.9	590	4	US-08-758-757-2
27	1206.5	38.9	590	5	PCT-US96-00996-5

28 1206.5 38.9 609 4 US-09-186-949A-2
29 1164.5 37.5 579 1 US-08-448-196A-8
30 1055 34.0 599 1 US-08-222-619-2
31 1055 34.0 599 3 US-08-221-767-24
32 1055 34.0 599 5 PCT-US95-04075-2
33 926 29.8 393 2 US-08-377-309-7
34 926 29.8 393 3 US-09-186-723-7
35 926 29.8 393 4 US-08-505-012-10
36 926 29.8 393 4 US-09-186-949A-8
37 926 29.8 393 4 US-08-758-757-7
38 926 29.8 393 5 PCT-US96-00996-10
39 777 25.0 324 4 US-08-505-012-12
40 777 25.0 324 5 PCT-US96-00996-22
41 777 25.0 325 2 US-08-377-309-8
42 777 25.0 325 3 US-09-186-723-8
43 777 25.0 325 4 US-08-505-012-11
44 777 25.0 325 4 US-09-186-949A-9
45 777 25.0 325 4 US-08-758-757-8

ALIGNMENTS

RESULT 1
US-06-153-799-14
; Sequence 14, Application US/08153799
; Patent No. 5768883
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J
; APPLICANT: Goodey, Andrew R
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: R Hain Swope, BOC Health Care Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847975
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8909916.2
; FILING DATE: 29-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00650
; FILING DATE: 26-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/775952
; FILING DATE: 29-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R Hain
; REGISTRATION NUMBER: 24864
; REFERENCE/DOCKET NUMBER: 92H832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 655 2400
; TELEFAX: (908) 771 6159
; TELEX: 219484
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Sequence 2, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 24, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 9, Appli
Sequence 8, Appli

```

; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Region
; LOCATION: 369..419
; OTHER INFORMATION: /note="Alternative C-termini of
; OTHER INFORMATION: HSA(1-n)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..585
; OTHER INFORMATION: /note="Amino acid sequence of
; OTHER INFORMATION: natural HSA"
US-08-153-799-14

Query Match 100.0%; Score 3103; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.3e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOQPFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOQPFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDNNPLRLVPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDNNPLRLVPEV 120
QY 121 DVMTCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAAKAAACLLP 180
DB 121 DVMTCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAAKAAACLLP 180
QY 181 KLDELDRDEGKASSAKQRLKASLOKFGERAFAKAWAVARLSORFFKAFPAEVSUKLVTLTK 240
DB 181 KLDELDRDEGKASSAKQRLKASLOKFGERAFAKAWAVARLSORFFKAFPAEVSUKLVTLTK 240
QY 241 VHTCCHGDLLECADRADLAKYICENODSISKKLKECCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCHGDLLECADRADLAKYICENODSISKKLKECCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMFLYFYARRHPDYVSVLLRLAKTYETTLTK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMFLYFYARRHPDYVSVLLRLAKTYETTLTK 360
QY 361 CAADPHECYAKVDFEFPKPLVEEPQNLKQNCLEFQQLGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHECYAKVDFEFPKPLVEEPQNLKQNCLEFQQLGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKKHPKAMPKCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKKHPKAMPKCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDVETYPKPFNAETFTTFHADICTLSEKERQIKKQALVELVGHKPKAT 540
DB 481 LVNRRPCFSALEVDVETYPKPFNAETFTTFHADICTLSEKERQIKKQALVELVGHKPKAT 540

```

RESULT 2

```

US-08-702-572-2
; Sequence 2, Application US/08702572
; Patent No. 5965386
; GENERAL INFORMATION:
; APPLICANT: Kerty-Williams, Sean M
; APPLICANT: Gilbert, Sarah C
; TITLE OF INVENTION: Yeast Strains and Modified Albumins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Centeon L.L.C.
; STREET: 1020 First Avenue

```

```

; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,572
; FILING DATE: 11-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/23857
; FILING DATE: 1-MAR-1995
; APPLICATION NUMBER: GB 9404270.2
; FILING DATE: 5-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Naomi Biswas
; REGISTRATION NUMBER: 38,384
; REFERENCE/DOCKET NUMBER: CE0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610/878/4294
; TELEFAX: 610/878/4221
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-572-2

```

```

Query Match 100.0%; Score 3103; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 9.3e-287;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOQPFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOQPFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDNNPLRLVPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDNNPLRLVPEV 120
QY 121 DVMTCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAAKAAACLLP 180
DB 121 DVMTCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAAKAAACLLP 180
QY 181 KLDELDRDEGKASSAKQRLKASLOKFGERAFAKAWAVARLSORFFKAFPAEVSUKLVTLTK 240
DB 181 KLDELDRDEGKASSAKQRLKASLOKFGERAFAKAWAVARLSORFFKAFPAEVSUKLVTLTK 240
QY 241 VHTCCHGDLLECADRADLAKYICENODSISKKLKECCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCHGDLLECADRADLAKYICENODSISKKLKECCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMFLYFYARRHPDYVSVLLRLAKTYETTLTK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMFLYFYARRHPDYVSVLLRLAKTYETTLTK 360
QY 361 CAADPHECYAKVDFEFPKPLVEEPQNLKQNCLEFQQLGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHECYAKVDFEFPKPLVEEPQNLKQNCLEFQQLGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKKHPKAMPKCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKKHPKAMPKCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDVETYPKPFNAETFTTFHADICTLSEKERQIKKQALVELVGHKPKAT 540
DB 481 LVNRRPCFSALEVDVETYPKPFNAETFTTFHADICTLSEKERQIKKQALVELVGHKPKAT 540

```

QY 541 KEOLKAVMDFFAFAVEKCKKADDDKTCFAEKGKLVAAQAALGL 585
 DB 541 KEOLKAVMDFFAFAVEKCKKADDDKTCFAEKGKLVAAQAALGL 585
 RESULT 3
 US-08-769-746-2
 ; Sequence 2, Application US/08769746
 ; Patent No. 6274305
 ; GENERAL INFORMATION:
 ; APPLICANT: Sonnenschein, Carlos
 ; APPLICANT: Soto, Ana M.
 ; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Medlen & Carroll, LLP
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent-In Release #1.0, Version #1.10
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/769,746
 ; FILING DATE: 19-DEC-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Carroll, Peter G.
 ; REGISTRATION NUMBER: 32,837
 ; REFERENCE/DOCKET NUMBER: MBR1-02584
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 705-8410
 ; TELEFAX: (415) 397-8338
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 585 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-769-746-2

Query Match 100.0%; Score 3103; DB 3; Length 585;
 Best Local Similarity 100.0%; Pred. NO. 9.3e-287;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDLGKLVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
 DB 1 DAHSEVAHRFKDLGKLVIAFAQYLOQCPEDHVKLVNEVTEFAKTCVADESAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCAKOEPRNECFLOHKKDDNPNLRLVRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCAKOEPRNECFLOHKKDDNPNLRLVRPEV 120
 QY 121 DVMCTAFHDNEETFLKYLVEIAERHPYFYAPELLFFAKRYKAAFTCCOAAKACLLP 180
 DB 121 DVMCTAFHDNEETFLKYLVEIAERHPYFYAPELLFFAKRYKAAFTCCOAAKACLLP 180
 QY 181 KLDELREGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSKLVLDLTK 240
 DB 181 KLDELREGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSKLVLDLTK 240
 QY 241 VHTCCGGHDLLEADRADLAKYICENQDSISSKLKCECKPLEKSHCIAVENDEMPA 300
 DB 241 VHTCCGGHDLLEADRADLAKYICENQDSISSKLKCECKPLEKSHCIAVENDEMPA 300
 QY 301 DLPSLAADFVESKVCXKVAEAKDVFGLMELYEARHPDYSVVLLRLAKTYETTLK 360
 DB 301 DLPSLAADFVESKVCXKVAEAKDVFGLMELYEARHPDYSVVLLRLAKTYETTLK 360

QY 361 CAADPHCEYAKVDFEFKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKYPOVST 420
 DB 361 CAADPHCEYAKVDFEFKPLVEEPQNLIKONCELFQOLGEYKFQNALLVRYTKYPOVST 420
 QY 421 PTLVEVSRLNGLKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRLNGLKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKFNFAETFTFHADICTLSEKERQIKKOTALVELVKGKPKAT 540
 DB 481 LVNRRPCFSALEVDETYVPKFNFAETFTFHADICTLSEKERQIKKOTALVELVKGKPKAT 540
 QY 541 KEOLKAVMDFFAFAVEKCKKADDDKTCFAEKGKLVAAQAALGL 585
 DB 541 KEOLKAVMDFFAFAVEKCKKADDDKTCFAEKGKLVAAQAALGL 585
 RESULT 4
 US-08-797-689-2
 ; Sequence 2, Application US/08797689
 ; Patent No. 5878969
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleer, Reinhard
 ; APPLICANT: Fournier, Alain
 ; APPLICANT: Guitton, Jean-Dominique
 ; APPLICANT: Jung, Gerard
 ; APPLICANT: Yeh, Patrice
 ; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 ; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.1 (patentIn)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/797,689
 ; FILING DATE: 31-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/256,927
 ; FILING DATE: 28-JUL-1994
 ; APPLICATION NUMBER: FR 92/01064
 ; FILING DATE: 31-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR93/00085
 ; FILING DATE: 28-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith Ph.D., Julie K.
 ; REGISTRATION NUMBER: P-38,619
 ; REFERENCE/DOCKET NUMBER: ST92006-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3839
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 610 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-797-689-2

Query Match 100.0%; Score 3103; DB 2; Length 610;
 Best Local Similarity 100.0%; Pred. NO. 9.8e-287;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 DAHSEVAHRFKDLEENFKALVLIAPQYLQOCPECHVHLVNEVTEFAKTCVADESAE 60
Db 25 DAHSEVAHRFKDLEENFKALVLIAPQYLQOCPECHVHLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGENADCCAKOEPRNECFLOHKDDNPNLPRVLRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGENADCCAKOEPRNECFLOHKDDNPNLPRVLRPEV 144
QY 121 DVNCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 145 DVNCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 204
QY 181 KLDELREGKASSAKORLKCASLOKFGERAFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 240
Db 205 KLDELREGKASSAKORLKCASLOKFGERAFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTLEK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTLEK 384
QY 361 CAADPHCEYAKVDFEKFPLVEEPONLIKONCELFEOQGEYKFNALLVRYTKVPQVST 420
Db 385 CAADPHCEYAKVDFEKFPLVEEPONLIKONCELFEOQGEYKFNALLVRYTKVPQVST 444
QY 421 PTLVEVSRNLGKVGSKCKCHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKCHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQOTALVELVHKHPKAT 540
Db 505 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQOTALVELVHKHPKAT 564
QY 541 KEQLKAVMDDPFAAFVEKCKCCKADDETCFAEBGKKLVAASQAALGL 585
Db 565 KEQLKAVMDDPFAAFVEKCKCCKADDETCFAEBGKKLVAASQAALGL 609
```

RESULT 5

```
US-08-256-938-2
; Sequence 2, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcoia Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
```

```
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-256-938-2
```

```
Query Match 100.0%; Score 3103; DB 1; Length 783;
Best Local Similarity 100.0%; Pred No. 1,4e-286;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFKDLEENFKALVLIAPQYLQOCPECHVHLVNEVTEFAKTCVADESAE 60
Db 25 DAHSEVAHRFKDLEENFKALVLIAPQYLQOCPECHVHLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGENADCCAKOEPRNECFLOHKDDNPNLPRVLRPEV 120
Db 85 NCDKSLHTLFGDKLCTVATLRETYGENADCCAKOEPRNECFLOHKDDNPNLPRVLRPEV 144
QY 121 DVNCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 145 DVNCTAFHDNEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 204
QY 181 KLDELREGKASSAKORLKCASLOKFGERAFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 240
Db 205 KLDELREGKASSAKORLKCASLOKFGERAFAKAWAVARLSQRFPKAEFAEVSCLVTDLT 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
Db 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTLEK 360
Db 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTLEK 384
QY 361 CAADPHCEYAKVDFEKFPLVEEPONLIKONCELFEOQGEYKFNALLVRYTKVPQVST 420
Db 385 CAADPHCEYAKVDFEKFPLVEEPONLIKONCELFEOQGEYKFNALLVRYTKVPQVST 444
QY 421 PTLVEVSRNLGKVGSKCKCHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 445 PTLVEVSRNLGKVGSKCKCHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQOTALVELVHKHPKAT 540
Db 505 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKEROIKKQOTALVELVHKHPKAT 564
QY 541 KEQLKAVMDDPFAAFVEKCKCCKADDETCFAEBGKKLVAASQAALGL 585
Db 565 KEQLKAVMDDPFAAFVEKCKCCKADDETCFAEBGKKLVAASQAALGL 609
```

RESULT 6

```
US-08-256-938-4
; Sequence 4, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcoia Road, 3C43
; CITY: Collegeville
; STATE: PA
```


COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (PatentIn)
CURRENT APPLICATION DATA:
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA: US/08/797,689
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1992
CLASSIFICATION: 435
PR-OR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-938-4

Query Match 100.0%; Score 3103; DB 1; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.4e-286;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSVAHREKDLGKLVIAFAQYLOQCPEFHVKLVNEVTEFAKTCVADESSE 60
DB 203 DAHKSVAHREKDLGKLVIAFAQYLOQCPEFHVKLVNEVTEFAKTCVADESSE 262

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVREVE 120
DB 263 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVREVE 322

QY 121 DVMCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 180
DB 323 DVMCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 382

QY 181 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVDTLTK 240
DB 383 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVDTLTK 442

QY 241 VHTCCHGDLLECAADRADLAKYICENQDISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
DB 443 VHTCCHGDLLECAADRADLAKYICENQDISSKLKECCEKPLLEKSHCIAEVENDEMPA 502

QY 301 DLPSLAADPVESKDVCKNTAEAKDVPLGMFLVEYARRHPDYSVVLRLRIAKTYETTLBKC 360
DB 503 DLPSLAADPVESKDVCKNTAEAKDVPLGMFLVEYARRHPDYSVVLRLRIAKTYETTLBKC 562

QY 361 CAAADPHECYAKVDFEFKPLVSEPNOLIKONCELFQELGEYFQNALVRYTKYPOVST 420
DB 563 CAAADPHECYAKVDFEFKPLVSEPNOLIKONCELFQELGEYFQNALVRYTKYPOVST 622

QY 421 PTLVEYSRNLGKVGSKCKHPBAKMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 480
DB 623 PTLVEYSRNLGKVGSKCKHPBAKMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES 682

QY 481 LVNRRPCFSALEVDETYVPKFNASTFTTHADICTLSEKEROIKKQATALVELVGHKPKAT 540
DB 683 LVNRRPCFSALEVDETYVPKFNASTFTTHADICTLSEKEROIKKQATALVELVGHKPKAT 742

QY 541 KSQLKAWMDQFAAFVEKCKCADDKCTCFAEEGKLVAAASQAALG 585
DB 743 KSQLKAWMDQFAAFVEKCKCADDKCTCFAEEGKLVAAASQAALG 787

RESULT 7
US-08-797-689-16
; Sequence 16, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fournier, Alain
; APPLICANT: Guitton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA: US/08/797,689
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1992
; CLASSIFICATION: 435
; PR-OR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-797-689-16

Query Match 100.0%; Score 3103; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.4e-286;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSVAHREKDLGKLVIAFAQYLOQCPEFHVKLVNEVTEFAKTCVADESSE 60
DB 203 DAHKSVAHREKDLGKLVIAFAQYLOQCPEFHVKLVNEVTEFAKTCVADESSE 262

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVREVE 120
DB 263 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVREVE 322

QY 121 DVMCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 180
DB 323 DVMCTAFHNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 382

QY 181 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVDTLTK 240
DB 383 KLDELDEGKASSAKORLKASLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVDTLTK 442

QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKEPLKSHCHIAEVENDEMPA 300
DB 443 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKEPLKSHCHIAEVENDEMPA 502
QY 301 DLPSLAADFVESKDVCKVKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTTLEKC 360
DB 503 DLPSLAADFVESKDVCKVKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTTLEKC 562
QY 361 CAADPHCEYAKVDFEFPKPLVEEPQNLIKONCELFQOLGYSKFQNALLVRYTKVPOVST 420
DB 563 CAADPHCEYAKVDFEFPKPLVEEPQNLIKONCELFQOLGYSKFQNALLVRYTKVPOVST 622
QY 421 PTLVEVSRLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRVTKCCTES 480
DB 623 PTLVEVSRLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRVTKCCTES 662
QY 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKERQIKKQALVELVKKPKAT 540
DB 683 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKERQIKKQALVELVKKPKAT 742
QY 541 KEQLKAVMDFFAAFEVKCKCKADOKETCFABEGKKLVAASQAALGL 585
DB 743 KEQLKAVMDFFAAFEVKCKCKADOKETCFABEGKKLVAASQAALGL 787

RESULT 8
US-08-222-619-3
; Sequence 3, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichensstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/222.619
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-222-619-3

Query Match 99.9%; Score 3099; DB 1; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.4e-286;
Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVLIAPYQLOQCFEDHVKLVNVEVTEFAKTCVADESA 60
DB 25 DAHKEVAHRFKDLGEENFKALVLIAPYQLOQCFEDHVKLVNVEVTEFAKTCVADESA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPPERNECFLOHKDNPPLVPRPEV 120

DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPPERNECFLOHKDNPPLVPRPEV 144
QY 121 DVMCTAFHDEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAFTSCCOAADAACCLP 180
DB 145 DVMCTAFHDEETFLKYLVEIARRHPYFYAPPELLFFAKRYKAFTSCCOAADAACCLP 204
QY 181 KLDELDEGKASSAKQRLKCSAQKQGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
DB 205 KLDELDEGKASSAKQRLKCSAQKQGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKEPLKSHCHIAEVENDEMPA 300
DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKCECKEPLKSHCHIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKVKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTTLEKC 360
DB 325 DLPSLAADFVESKDVCKVKNYAEAKDVFLGMFLYEVARRHPDYSVVLRLAKTYETTTLEKC 384
QY 361 CAADPHCEYAKVDFEFPKPLVEEPQNLIKONCELFQOLGYSKFQNALLVRYTKVPOVST 420
DB 385 CAADPHCEYAKVDFEFPKPLVEEPQNLIKONCELFQOLGYSKFQNALLVRYTKVPOVST 444
QY 421 PTLVEVSRLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRVTKCCTES 480
DB 445 PTLVEVSRLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKERQIKKQALVELVKKPKAT 540
DB 505 LVNRRPCFSALEVDYTYVPKEFNAETFTFHADICTLSEKERQIKKQALVELVKKPKAT 564
QY 541 KEQLKAVMDFFAAFEVKCKCKADOKETCFABEGKKLVAASQAALGL 585
DB 565 KEQLKAVMDFFAAFEVKCKCKADOKETCFABEGKKLVAASQAALGL 609

RESULT 9
US-08-433-037-4
; Sequence 4, Application US/08433037
; Patent No. 5707828
; GENERAL INFORMATION:
; APPLICANT: Sreekrishna, Kotikanyadan
; APPLICANT: Barr, Kathryn A.
; APPLICANT: Brietley, Russell A.
; APPLICANT: Thill, Gregory P.
; APPLICANT: Tschopp, Juerg P.
; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
; TITLE OF INVENTION: PICHIA PASTORIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/433.037
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 91082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-037-4

Query Match 99.9%; Score 3099; DB 1; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.4e-286;
Matches 584; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAHKSEVAHREFKDLGLENFKALVLIAPFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 60
DB 25 DAHKSEVAHREFKDLGLENFKALVLIAPFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 144
QY 121 DVNCTAFHNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 180
DB 145 DVNCTAFHNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 204
QY 181 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
DB 205 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK 360
DB 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK 384
QY 361 CAAADPHCEYAKVDFBPKLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 420
DB 385 CAAADPHCEYAKVDFBPKLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDYTPVKPFNAETFTFHADICTLSEKERQIKKOTALVELVHKHKPKAT 540
DB 505 LVNRRPCFSALEVDYTPVKPFNAETFTFHADICTLSEKERQIKKOTALVELVHKHKPKAT 564
QY 541 KEQLKAVMDDFAAFVEKCKCCKADDKETCFABEGKKLVAASQAALGL 585
DB 565 KEQLKAVMDDFAAFVEKCKCCKADDKETCFABEGKKLVAASQAALGL 609

RESULT 10
US-08-897-956A-2
Sequence 2, Application US/08897956A
Patent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Hermann Gram
TITLE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/GPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 609
TYPE: PRT
ORGANISM: Homo Sapiens
US-08-897-956A-2

Query Match 99.9%; Score 3099; DB 4; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.4e-286;
Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHREFKDLGLENFKALVLIAPFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 60
DB 25 DAHKSEVAHREFKDLGLENFKALVLIAPFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 144
QY 121 DVNCTAFHNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 180
DB 145 DVNCTAFHNEETFLKKYLVEIARRHPYFYAPPELLFFAKRYKAAFTCCCAADKAAACLLP 204
QY 181 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
DB 205 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTK 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK 360
DB 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK 384
QY 361 CAAADPHCEYAKVDFBPKLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 420
DB 385 CAAADPHCEYAKVDFBPKLVEEPQNLKQNCFLFQOLGEYKFNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEVSRLNGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDYTPVKPFNAETFTFHADICTLSEKERQIKKOTALVELVHKHKPKAT 540
DB 505 LVNRRPCFSALEVDYTPVKPFNAETFTFHADICTLSEKERQIKKOTALVELVHKHKPKAT 564
QY 541 KEQLKAVMDDFAAFVEKCKCCKADDKETCFABEGKKLVAASQAALGL 585
DB 565 KEQLKAVMDDFAAFVEKCKCCKADDKETCFABEGKKLVAASQAALGL 609

RESULT 1:
PCT-US95-04075-3
Sequence 3, Application PC/TUS9504075
GENERAL INFORMATION:
APPLICANT: AMGEN INC.
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/PRC
STREET: 1840 DeHavilland Drive
City: Thousand Oaks
STATE: California
COUNTRY: U.S.
Zip: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids

; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US95-04075-3

Query Match 99.9%; Score 3099; DB 5; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.4e-286;
Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 3;

QY 1 DAHKSEVAHRFKDLGEENFKALVLIAPAYIQQQPFEDHVKLVNVEVTEFAKTCVADESAS 60
DB 25 DAHKSEVAHRFKDLGEENFKALVLIAPAYIQQQPFEDHVKLVNVEVTEFAKTCVADESAS 84
QY 61 NDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNPMLPLVRPEV 120
DB 85 NDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNPMLPLVRPEV 144
QY 121 DVMCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 180
DB 145 DVMCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 204
QY 181 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAKFAEVSCLVTLTK 240
DB 205 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAKFAEVSCLVTLTK 264
QY 241 VHTCCHGDLLECADRADLAKYICENODS:SSKLKECEKPLLEKSHCIAEVENDEMPA 300
DB 265 VHTCCHGDLLECADRADLAKYICENODS:SSKLKECEKPLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADPVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYVSVLLRLAKTYETTLK 360
DB 325 DLPSLAADPVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYVSVLLRLAKTYETTLK 384
QY 361 CAADPHECYAKVDFEPLVEEPQNLIKQNCLEPEQLGEYKFNALLVRYTKVQVST 420
DB 385 CAADPHECYAKVDFEPLVEEPQNLIKQNCLEPEQLGEYKFNALLVRYTKVQVST 444
QY 421 PTLVEVSRNLGKVGSKCKKHPEAKMPCAEADYLSVNLQCLVLEKTPVSDRVTKCCTES 480
DB 445 PTLVEVSRNLGKVGSKCKKHPEAKMPCAEADYLSVNLQCLVLEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVHKPKAT 540
DB 505 LVNRRPCFSALVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVHKPKAT 564
QY 541 KEQLKAVMDDFAAFAVEKCKKADDKETCFAEEGKKLVAAASQAALGL 585
DB 565 KEQLKAVMDDFAAFAVEKCKKADDKETCFAEEGKKLVAAASQAALGL 609

RESULT 12

US-08-897-956A-3
; Sequence 3, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide

US-08-897-956A-3

Query Match 99.7%; Score 3095; DB 4; Length 978;
Best Local Similarity 99.8%; Pred. No. 1.1e-285;
Matches 583; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVLIAPAYIQQQPFEDHVKLVNVEVTEFAKTCVADESAS 60
DB 212 DAHKSEVAHRFKDLGEENFKALVLIAPAYIQQQPFEDHVKLVNVEVTEFAKTCVADESAS 271
QY 61 NDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNPMLPLVRPEV 120
DB 272 NDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNPMLPLVRPEV 331
QY 121 DVMCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 180
DB 332 DVMCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 391
QY 181 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAKFAEVSCLVTLTK 240
DB 392 KLDELDEGKASSAKQRLKCAASLQKFGERAFKAWAVARLSQRFPAKFAEVSCLVTLTK 451
QY 241 VHTCCHGDLLECADRADLAKYICENODS:SSKLKECEKPLLEKSHCIAEVENDEMPA 300
DB 452 VHTCCHGDLLECADRADLAKYICENODS:SSKLKECEKPLLEKSHCIAEVENDEMPA 511
QY 301 DLPSLAADPVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYVSVLLRLAKTYETTLK 360
DB 512 DLPSLAADPVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYVSVLLRLAKTYETTLK 571
QY 361 CAADPHECYAKVDFEPLVEEPQNLIKQNCLEPEQLGEYKFNALLVRYTKVQVST 420
DB 572 CAADPHECYAKVDFEPLVEEPQNLIKQNCLEPEQLGEYKFNALLVRYTKVQVST 631
QY 421 PTLVEVSRNLGKVGSKCKKHPEAKMPCAEADYLSVNLQCLVLEKTPVSDRVTKCCTES 480
DB 632 PTLVEVSRNLGKVGSKCKKHPEAKMPCAEADYLSVNLQCLVLEKTPVSDRVTKCCTES 691
QY 481 LVNRRPCFSALVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVHKPKAT 540
DB 692 LVNRRPCFSALVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVHKPKAT 751
QY 541 KEQLKAVMDDFAAFAVEKCKKADDKETCFAEEGKKLVAAASQAALG 584
DB 752 KEQLKAVMDDFAAFAVEKCKKADDKETCFAEEGKKLVAAASQAALG 795

RESULT 13

US-08-448-196A-3
; Sequence 3, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: RELATED PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIP: 35812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: BROAD JR., ROBERT L.
 REGISTRATION NUMBER: 18,757
 REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 205-544-0021
 TELEFAX: 205-544-0258
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 585 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-448-196A-3

Query Match 99.7%; Score 3093; DB 1; Length 585;
 Best Local Similarity 99.7%; Pred. No. 8.3e-286;
 Matches 583; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGEENFKALVLIIFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHFRKDLGEENFKALVLIIFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEERNECFLOHKDDNPNLRLVRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEERNECFLOHKDDNPNLRLVRPEV 120
 QY 121 DVMTAFPHDNEETFLKYLVEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
 DB 121 DVMTAFPHDNEETFLKYLVEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKACASLOKFGERAFAKAWAVARLSORFPKAEFAEVSCLVTDLT 240
 DB 181 KLDELDEGKASSAKORLKACASLOKFGERAFAKAWAVARLSORFPKAEFAEVSCLVTDLT 240
 QY 241 VHTTECHGDLLECCADDDRADLAKYICENODSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
 DB 241 VHTTECHGDLLECCADDDRADLAKYICENODSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKVCNKYAEAKDVFLGMFLYAEARRHPDYSVVLLRLAKTYETTTLEKC 360
 DB 301 DLPSLAADFVESKVCNKYAEAKDVFLGMFLYAEARRHPDYSVVLLRLAKTYETTTLEKC 360
 QY 361 CAADHPHECYAKVDFEFPKPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 DB 361 CAADHPHECYAKVDFEFPKPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
 DB 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
 QY 541 KEQLKAVMDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585
 DB 541 KEQLKAVMDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585

RESULT 14
 US-08-984-176-1
 Sequence 1, Application: US/08984176
 Patent No. 5948609
 GENERAL INFORMATION:
 APPLICANT: CARTER, DANIEL C
 APPLICANT: HO, JOSEPH X
 APPLICANT: RUKER, FLORIAN
 TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT
 TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER

FILE REFERENCE: 08/984,176
 CURRENT APPLICATION NUMBER: US/08/984,176
 CURRENT FILING DATE: 1997-12-03
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 585
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-984-176-1

Query Match 99.7%; Score 3093; DB 2; Length 585;
 Best Local Similarity 99.7%; Pred. No. 8.3e-286;
 Matches 583; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAHSEVAHFRKDLGEENFKALVLIIFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHFRKDLGEENFKALVLIIFAQYLOQCPFDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEERNECFLOHKDDNPNLRLVRPEV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPEERNECFLOHKDDNPNLRLVRPEV 120
 QY 121 DVMTAFPHDNEETFLKYLVEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
 DB 121 DVMTAFPHDNEETFLKYLVEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKACASLOKFGERAFAKAWAVARLSORFPKAEFAEVSCLVTDLT 240
 DB 181 KLDELDEGKASSAKORLKACASLOKFGERAFAKAWAVARLSORFPKAEFAEVSCLVTDLT 240
 QY 241 VHTTECHGDLLECCADDDRADLAKYICENODSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
 DB 241 VHTTECHGDLLECCADDDRADLAKYICENODSISSKLKCECEKPLLEKSHCIAEVENDEMPA 300
 QY 301 DLPSLAADFVESKVCNKYAEAKDVFLGMFLYAEARRHPDYSVVLLRLAKTYETTTLEKC 360
 DB 301 DLPSLAADFVESKVCNKYAEAKDVFLGMFLYAEARRHPDYSVVLLRLAKTYETTTLEKC 360
 QY 361 CAADHPHECYAKVDFEFPKPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 DB 361 CAADHPHECYAKVDFEFPKPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
 QY 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 421 PTLVEVSRNLGKVGSKCCCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
 DB 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
 QY 541 KEQLKAVMDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585
 DB 541 KEQLKAVMDDFAAFVEKCKKADDDKTCFAEBEGKKLVAASQAALGL 585

RESULT 15
 US-08-448-196A-5
 Sequence 5, Application: US/08448196A
 Patent No. 5780594
 GENERAL INFORMATION:
 APPLICANT: CARTER, DANIEL C
 TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
 TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
 TITLE OF INVENTION: RELATED PROTEINS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NASA
 STREET: MARSHALL SPACE FLIGHT CENTER
 CITY: HUNTSVILLE
 STATE: ALABAMA
 COUNTRY: USA
 ZIP: 35812

Job time : 32 secs

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROAD JR., ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEFAX: 205-544-0258
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-448-196A-5

Query Match 79.2%; Score 2458.5; DB 1; Length 583;
Best Local Similarity 75.8%; Pred. No. 2.1e-225;
Matches 442; Conservative 70; Mismatches 70; Indels 1; Gaps 1;

QY 1 DAHSEVAHREFKDLGEENFKALVLIATAQYLQOCFFEDHVKLVNEVTEFAKTCVADESAE 60
DB 1 DTHKSEIAHRNDLGEKHFGLVLVAQSQYLQOCFFEDHVKLVNEVTEFAKTCVADESAE 60

QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLK-KPEP 119

QY 121 DVMCTAFHNDSETFLKLYLRIARRHPYFAPELIFFAKRYKAAFTCCCAADKACCLLP 180
DB 120 DAQCAAFQEDPKFLGKLYEVARRHPYFYPELLFHAEEYKADFTECCPADDKLACLP 179

QY 181 KLDELRLDEGKASSAKQRLKASQLOKFGERAFKAWAVARLSQRPFAEFAEYKLVTDLT 240
DB 180 KLDALKERILLSSAKERLKCSSFQNFGERAVKANSVARLSQKPKADFAEVSKIIVDTLT 239

QY 241 VHTCECHGDLLECADDRADLAKYICENODSISSKLKECCEKPLEKSHCIAEYENDEMPA 300
DB 240 VHKECCHGDLLECADDRADLAKYICEHODS-SGKLKACCDKPLQKSHCIAEYKEDDLPS 299

QY 301 DLPSSAADFVESKDYCKNVYAKQVFLGMFLYEVARRHPDYSVLLRLAKTYETTLK 360
DB 300 DIPALAAADFADKEICKHYKQAKQVFLGTFLEYYSRRHPDYSVLLRLAKTYEATLEK 359

QY 361 CAADPHCEYAKVDFEPKPLVEEPONLIKQNCLEFQELGEYKFNALLVRYTKVPOVST 420
DB 360 CAEADPPACYRTVFQDTPLVVEEPKSLVKQNCDFEEVGEYDFQNALIVRYTKKAPQVST 419

QY 421 PTLVEVSNLGVKSGKCKHPKPEAKMPCAEYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 420 PTLVEIGRTLGVKSGRCCKLPSEERLPCSENHLAALNRCLVULHEKTPVSEKIKKCTDS 479

QY 481 LVNRRPCFSALEVEITYVPKEFNAETFTFHADICTLSEKERQIKKQIALVELVHKPKAT 540
DB 480 LAERRPCFSALEDEGYVPKFEKATFTFHADICTLPEDEKQIKKQSAELVVKHKPKAT 539

QY 541 KEQLKAVMDDFAAFVEKCKADDKETCFABEGKLVVAASQAL 583
DB 540 KEQLKTVLGNFSAFVAKCCGREDKACFAEBGPKLVASSQAL 582
```

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	3103	100.0	585	10	US-09-929-552-2	Sequence	
2	3103	100.0	585	11	US-09-932-613-445	Sequence	
3	3103	100.0	585	11	US-09-984-010-26	Sequence	
4	3103	100.0	585	11	US-09-833-041-18	Sequence	
5	3103	100.0	585	12	US-10-153-604A-5	Sequence	
6	3103	100.0	585	12	US-09-833-117-18	Sequence	
7	3103	100.0	585	12	US-10-319-263-1	Sequence	
8	3103	100.0	585	12	US-10-319-263-2	Sequence	
9	3103	100.0	585	12	US-10-414-469-1	Sequence	
10	3103	100.0	585	12	US-10-414-469-2	Sequence	
11	3103	100.0	585	12	US-09-932-322-445	Sequence	
12	3103	100.0	585	12	US-10-413-831-1	Sequence	
13	3103	100.0	585	12	US-10-413-831-2	Sequence	
14	3103	100.0	585	14	US-10-153-064-5	Sequence	
15	3103	100.0	604	11	US-09-984-010-7	Sequence	

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-929-552-2

Query Match      100.0%; Score 3103; DB 10; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHREFKDLGEENFKALVLIATFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHSEVAHREFKDLGEENFKALVLIATFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLTRETYGEMADCCAKOEPEKNECFLOHKDNDNPLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLTRETYGEMADCCAKOEPEKNECFLOHKDNDNPLRLVRPEV 120
QY 121 DVMTAFHDNDETFLLKYLVEIARRHPYFYAPPELLFTAKRYKAAFTCCQAAADKAAACLLP 180
DB 121 DVMTAFHDNDETFLLKYLVEIARRHPYFYAPPELLFTAKRYKAAFTCCQAAADKAAACLLP 180
QY 181 KLDELURDEGKASSAKQRLKCSLQKFGGERAFKAWAVARLSQRPFAEFAEVSCLVTDLTK 240
DB 181 KLDELURDEGKASSAKQRLKCSLQKFGGERAFKAWAVARLSQRPFAEFAEVSCLVTDLTK 240
QY 241 VHTTECHGDLLECADDDRADLAKYICENQDSISSKLKECCCKPLLEKSHCIAEVENDEMPA 300
DB 241 VHTTECHGDLLECADDDRADLAKYICENQDSISSKLKECCCKPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYABAKDVFGLMFLYEYARRHPDYSVVLLRLAKTYETTLK 360
DB 301 DLPSLAADFVESKDVCKNYABAKDVFGLMFLYEYARRHPDYSVVLLRLAKTYETTLK 360
QY 361 CAADPHCYAKVDFEPKPLVEEPQNLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST 420
DB 361 CAADPHCYAKVDFEPKPLVEEPQNLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST 420
QY 421 PTLVEVSRLNGVSKCKCHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRLNGVSKCKCHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQATLVELVVKHKPKAT 540
DB 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQATLVELVVKHKPKAT 540
QY 541 KEQLKAVMDDFAAFVEKCKCKADDDKTCFAEBGKGLVAASQAALGL 585
DB 541 KEQLKAVMDDFAAFVEKCKCKADDDKTCFAEBGKGLVAASQAALGL 585

RESULT 3
US-09-984-010-26
; Sequence 26, Application US/09984010
; Publication No. US20030104578A1
; GENERAL INFORMATION:
; APPLICANT: Balliance, David James
; TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
; AND SERJM ALBUMIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPC)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,010
; FILING DATE: 21-May-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,873
; FILING DATE: 25-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03164

```


; FILING DATE: 19-DEC-1996
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-832-501-18

Query Match	100.0%	Score 3103;	DB 11;	Length 585;
Best Local Similarity	100.0%	Pred. No. 2.4e-269;		
Matches 585;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 3;

QY	1	DAHKSEVAHRFKDLGEENFKALVLI	FAQYLQCCPFEDHVKLVNEVTEFAKTCVADES	AE 60
DB	1	DAHKSEVAHRFKDLGEENFKALVLI	FAQYLQCCPFEDHVKLVNEVTEFAKTCVADES	AE 60
QY	61	NCDSLSHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL	PRLVRPEV	120
DB	61	NCDSLSHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL	PRLVRPEV	120
QY	121	DVMCTAFHDNEETFLKXYLYEIARRHPYFYAPELFFAKRYKAATFECQAADKAACLLP	180	
DB	121	DVMCTAFHDNEETFLKXYLYEIARRHPYFYAPELFFAKRYKAATFECQAADKAACLLP	180	
QY	181	KLDELREDEGKASSAKORLKASQKFGGERAFKAWAVARLSQRPFAEFVSKLVTDLTK	240	
DB	181	KLDELREDEGKASSAKORLKASQKFGGERAFKAWAVARLSQRPFAEFVSKLVTDLTK	240	
QY	241	VHTECHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA	300	
DB	241	VHTECHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA	300	
QY	301	DLPSLAADFVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK	360	
DB	301	DLPSLAADFVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK	360	
QY	361	CAAADPHECYAKVDFEKPPLVEEPQNLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST	420	
DB	361	CAAADPHECYAKVDFEKPPLVEEPQNLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST	420	
QY	421	PTLVEVSRNLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHLHEKTPVSDRVTKCCTES	480	
DB	421	PTLVEVSRNLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHLHEKTPVSDRVTKCCTES	480	
QY	481	LVNRRPCFSALEVDYTPVKEFNAETFTFHADICTLSEKERQIKQTALVELVKGKPKAT	540	
DB	481	LVNRRPCFSALEVDYTPVKEFNAETFTFHADICTLSEKERQIKQTALVELVKGKPKAT	540	

RESULT 4
US-09-833-041-18
; Sequence 18, Application US/09833041
; Publication No. US20030125247A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haeelintine, William A.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF545
; CURRENT APPLICATION NUMBER: US/09/833,041
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-833-041-18

Query Match	100.0%	Score 3103;	DB 11;	Length 585;
Best Local Similarity	100.0%	Pred. No. 2.4e-269;		
Matches 585;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 3;

QY	1	DAHKSEVAHRFKDLGEENFKALVLI	FAQYLQCCPFEDHVKLVNEVTEFAKTCVADES	AE 60
DB	1	DAHKSEVAHRFKDLGEENFKALVLI	FAQYLQCCPFEDHVKLVNEVTEFAKTCVADES	AE 60
QY	61	NCDSLSHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL	PRLVRPEV	120
DB	61	NCDSLSHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL	PRLVRPEV	120
QY	121	DVMCTAFHDNEETFLKXYLYEIARRHPYFYAPELFFAKRYKAATFECQAADKAACLLP	180	
DB	121	DVMCTAFHDNEETFLKXYLYEIARRHPYFYAPELFFAKRYKAATFECQAADKAACLLP	180	
QY	181	KLDELREDEGKASSAKORLKASQKFGGERAFKAWAVARLSQRPFAEFVSKLVTDLTK	240	
DB	181	KLDELREDEGKASSAKORLKASQKFGGERAFKAWAVARLSQRPFAEFVSKLVTDLTK	240	
QY	241	VHTECHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA	300	
DB	241	VHTECHGDLLECCADRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA	300	
QY	301	DLPSLAADFVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK	360	
DB	301	DLPSLAADFVESKQVCKNYAEAKOVFLGMFLYEVARRHPDYSVVLLRLAKTYETTLK	360	
QY	361	CAAADPHECYAKVDFEKPPLVEEPQNLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST	420	
DB	361	CAAADPHECYAKVDFEKPPLVEEPQNLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST	420	
QY	421	PTLVEVSRNLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHLHEKTPVSDRVTKCCTES	480	
DB	421	PTLVEVSRNLGKVGSKCKCKHPEAKRMPCAEDYLSVNLQCLVHLHEKTPVSDRVTKCCTES	480	
QY	481	LVNRRPCFSALEVDYTPVKEFNAETFTFHADICTLSEKERQIKQTALVELVKGKPKAT	540	
DB	481	LVNRRPCFSALEVDYTPVKEFNAETFTFHADICTLSEKERQIKQTALVELVKGKPKAT	540	
QY	541	KEQLKAVMDPFAAFVEKCCCKADKTCFAEEGKKLVAASQAALGL	585	
DB	541	KEQLKAVMDPFAAFVEKCCCKADKTCFAEEGKKLVAASQAALGL	585	

RESULT 5
US-10-153-604A-5
; Sequence 5, Application US/10153604A
; Publication No. US20030143191A1
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556
; CURRENT APPLICATION NUMBER: US/10/153,604A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens

US-10-153-604A-S

Query Match 100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHSEVAHRFKDLGEENFKALVLIATAFYAQYLOQCPEFHVKLVNEVTEFAKTCVADESAAE 60
Db 1 DAHSEVAHRFKDLGEENFKALVLIATAFYAQYLOQCPEFHVKLVNEVTEFAKTCVADESAAE 60

Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120

Qy 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
Db 121 DVNCTAFHNEETFLKKYLYEIAARRHPYFAPPELLFFAKRYKAAFTCCQAADKAACLLP 180

Qy 181 KLDELDEGKASSAKORLKASLQKGERAFKAWAVARLSORFPKAEFAEVSCLVTDLTJK 240
Db 181 KLDELDEGKASSAKORLKASLQKGERAFKAWAVARLSORFPKAEFAEVSCLVTDLTJK 240

Qy 241 VHTCCGDLLECCADDRADLAKYICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCGDLLECCADDRADLAKYICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPA 300

Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKC 360
Db 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKC 360

Qy 361 CAADPHECYAKVDFEFPKLVBEPPONLIKONCELFEOQGEYKFNALLVRYTKVQVQST 420
Db 361 CAADPHECYAKVDFEFPKLVBEPPONLIKONCELFEOQGEYKFNALLVRYTKVQVQST 420

Qy 421 PTLVEVSRNLGVKSGKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGVKSGKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

Qy 481 LVNRRPCFSALEVDETYVPKFNAAETFTFHADICTLSEKERQIKKOTALVELVGHKPKAT 540
Db 481 LVNRRPCFSALEVDETYVPKFNAAETFTFHADICTLSEKERQIKKOTALVELVGHKPKAT 540

Qy 541 KEQLKAVMDDFAAVFEKCKCADDKETCFABEGKKLVAASQAALGL 585
Db 541 KEQLKAVMDDFAAVFEKCKCADDKETCFABEGKKLVAASQAALGL 585

RESULT 6

US-09-833-117-18
; Sequence 18, Application US/09833117
; Publication No. US20030171267A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Sadeghi, Homa
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF543
; CURRENT APPLICATION NUMBER: US/09/833,117
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-833-117-18

RESULT 7

US-10-319-263-1
; Sequence 1, Application US/10319263
; Publication No. US20030180820A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or M.D., David
; APPLICANT: Lau Ph.D., Edward
; APPLICANT: Winkler M.D., James V.
; TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
; TITLE OF INVENTION: Kits
; FILE REFERENCE: ISC007
; CURRENT APPLICATION NUMBER: US/10/319,263
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/115,392
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: 60/102,738
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,926
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,581
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
;

US-10-319-263-1

Query Match 100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOCPFFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOCPFFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
QY 121 DVMTCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVMTCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELRLDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
DB 181 KLDELRLDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
QY 241 VHTCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMPLYEYARRHPDYSVVLLRLAKTYETTLTK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMPLYEYARRHPDYSVVLLRLAKTYETTLTK 360
QY 361 CAADAPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFKQNALLVRYTKVPQVST 420
DB 361 CAADAPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFKQNALLVRYTKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKCKHPEAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKCKHPEAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDETYVPKFNFAETFTFHADICTLSEKEROIKKQALVELVXHKPKAT 540
DB 481 LVNRRPCFSALEVDETYVPKFNFAETFTFHADICTLSEKEROIKKQALVELVXHKPKAT 540
QY 541 KEQLKAVMDDFAAAFVEKCKCKADKCTCFPAEKGKLVAAASQAALGL 585
DB 541 KEQLKAVMDDFAAAFVEKCKCKADKCTCFPAEKGKLVAAASQAALGL 585

RESULT 8

US-10-319-263-2
; Sequence 2, Application US/10319263
; Publication No. US20030180820A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or M.D., David
; APPLICANT: Lau Ph.D., Edward
; APPLICANT: Winkler M.D., James V.
; TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
; TITLE OF INVENTION: Kits
; FILE REFERENCE: ISCO07
; CURRENT APPLICATION NUMBER: US/10/319,263
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/115,392
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: 60/102,738
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,926
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,581
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 585
; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (1)..(585)

; OTHER INFORMATION: ACETYLTATION

US-10-319-263-2

Query Match 100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOCPFFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 1 DAHKEVAHRFKDLGEENFKALVLIAPAYLQOCPFFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEV 120
QY 121 DVMTCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
DB 121 DVMTCTAFHDNEETFLKKYLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
QY 181 KLDELRLDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
DB 181 KLDELRLDEGKASSAKQRLKCSLQKFGERAFKAWAVARLSORFPKAEFAEVSCLVTDLT 240
QY 241 VHTCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
DB 241 VHTCCHGDLLECADRADLAKYICENQDSISSKLKCECKEPPLLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMPLYEYARRHPDYSVVLLRLAKTYETTLTK 360
DB 301 DLPSLAADFVESKDVCKNYAEAKOVFLGMPLYEYARRHPDYSVVLLRLAKTYETTLTK 360
QY 361 CAADAPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFKQNALLVRYTKVPQVST 420
DB 361 CAADAPHECYAKVDFEPLVEEPQNLKQNCLEFQELGEYKFKQNALLVRYTKVPQVST 420
QY 421 PTLVEVSRNLGKVGSKCKCKHPEAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 421 PTLVEVSRNLGKVGSKCKCKHPEAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDETYVPKFNFAETFTFHADICTLSEKEROIKKQALVELVXHKPKAT 540
DB 481 LVNRRPCFSALEVDETYVPKFNFAETFTFHADICTLSEKEROIKKQALVELVXHKPKAT 540
QY 541 KEQLKAVMDDFAAAFVEKCKCKADKCTCFPAEKGKLVAAASQAALGL 585
DB 541 KEQLKAVMDDFAAAFVEKCKCKADKCTCFPAEKGKLVAAASQAALGL 585

RESULT 9

US-10-414-469-1
; Sequence 1, Application US/10414469
; Publication No. US20030190691A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or M.D., David
; APPLICANT: Lau Ph.D., Edward
; APPLICANT: Winkler M.D., James V.
; TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
; TITLE OF INVENTION: Kits
; FILE REFERENCE: ISCO07
; CURRENT APPLICATION NUMBER: US/10/414,469
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/806,247
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/US99/22905
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/115,392
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: 60/102,738
; PRIOR FILING DATE: 1998-10-02

; PRIOR APPLICATION NUMBER: 09/165,926
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,591
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-469-1

Query Match 100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKEVAHRFKDLGEENFKALVLIAPAYIQOCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 1 DAHKEVAHRFKDLGEENFKALVLIAPAYIQOCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
QY 121 DVMCTAFHNEETFLKKYLYEARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 180
Db 121 DVMCTAFHNEETFLKKYLYEARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRPFAEFAEVSKLVTDLTK 240
Db 181 KLDELDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRPFAEFAEVSKLVTDLTK 240
QY 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCPELLEKSHCIAEVENDEMPA 300
Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCPELLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADVESEKDVCKKNYAEAKDVFLGMFLYEVARRHPDYSVLLRLAKTYETTLK 360
Db 301 DLPSLAADVESEKDVCKKNYAEAKDVFLGMFLYEVARRHPDYSVLLRLAKTYETTLK 360
QY 361 CAAADPHECYAKVDFEFPLVEEPONLIKQNCLEGEQKQALVRYTKKVPQVST 420
Db 361 CAAADPHECYAKVDFEFPLVEEPONLIKQNCLEGEQKQALVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGVGSKCCCKHPKAMPKCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGVGSKCCCKHPKAMPKCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVXHKPKAT 540
Db 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVXHKPKAT 540
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDKETCTFAEBGKCLVAASQAALGL 585
Db 541 KEQLKAVMDDDFAAFVEKCKCKADDKETCTFAEBGKCLVAASQAALGL 585

RESULT 10

US-10-414-469-2
; Sequence 2, Application US/10414469
; Publication No. US20030190691A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or M.D., David
; APPLICANT: Lau Ph.D., Edward
; TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
; TITLE OF INVENTION: Kits
; FILE REFERENCE: ISC007
; CURRENT APPLICATION NUMBER: US/10/414,469
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/806,247
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/US99/22905

; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/115,392
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: 60/102,738
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,926
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,581
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(585)
; OTHER INFORMATION: ACETYLATION
US-10-414-469-2

Query Match 100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKEVAHRFKDLGEENFKALVLIAPAYIQOCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
Db 1 DAHKEVAHRFKDLGEENFKALVLIAPAYIQOCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPLVRPEV 120
QY 121 DVMCTAFHNEETFLKKYLYEARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 180
Db 121 DVMCTAFHNEETFLKKYLYEARRHPYFYAPPELLFFAKRYKAAPTECCQAADKAACLLP 180
QY 181 KLDELDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRPFAEFAEVSKLVTDLTK 240
Db 181 KLDELDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRPFAEFAEVSKLVTDLTK 240
QY 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCPELLEKSHCIAEVENDEMPA 300
Db 241 VHTTECHGDLLECADRADLAKYICENQDSISSKLKECCPELLEKSHCIAEVENDEMPA 300
QY 301 DLPSLAADVESEKDVCKKNYAEAKDVFLGMFLYEVARRHPDYSVLLRLAKTYETTLK 360
Db 301 DLPSLAADVESEKDVCKKNYAEAKDVFLGMFLYEVARRHPDYSVLLRLAKTYETTLK 360
QY 361 CAAADPHECYAKVDFEFPLVEEPONLIKQNCLEGEQKQALVRYTKKVPQVST 420
Db 361 CAAADPHECYAKVDFEFPLVEEPONLIKQNCLEGEQKQALVRYTKKVPQVST 420
QY 421 PTLVEVSRNLGVGSKCCCKHPKAMPKCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db 421 PTLVEVSRNLGVGSKCCCKHPKAMPKCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
QY 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVXHKPKAT 540
Db 481 LVNRRPCFSALEVDETYVPKFNAEFTTFHADICTLSEKERQIKKQATLVELVXHKPKAT 540
QY 541 KEQLKAVMDDDFAAFVEKCKCKADDKETCTFAEBGKCLVAASQAALGL 585
Db 541 KEQLKAVMDDDFAAFVEKCKCKADDKETCTFAEBGKCLVAASQAALGL 585

RESULT 11

US-09-932-322-445
; Sequence 445, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.

```
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)
; FILE REFERENCE: DXX-018.1 PCT; DXX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/832.322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 445
; LENGTH: 585
; TYPE: PRT
; ORGANISM: HomoSapiens
US-09-932-322-445

Query Match      100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGGEENFKALVLJAFAPQYLQOCPPFEDHVKLVNEVTEFAKTCVADSEAE 60
Db 1 DAHKSEVAHRFKDLGGEENFKALVLJAFAPQYLQOCPPFEDHVKLVNEVTEFAKTCVADSEAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDQNPRLPLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDQNPRLPLVRPEV 120
Qy 121 DVMTAFHNDNEETFLKYLVEIARRHPFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 121 DVMTAFHNDNEETFLKYLVEIARRHPFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Qy 181 KLDELDRSGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVDLT 240
Db 181 KLDELDRSGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVDLT 240
Qy 241 VHTCCGDLLECCADRADLAKYICENQDS:SSKLKECCCKPFLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCGDLLECCADRADLAKYICENQDS:SSKLKECCCKPFLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEVYARRHPDYSVLLRLAKTYETLEKC 360
Db 301 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEVYARRHPDYSVLLRLAKTYETLEKC 360
Qy 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
Db 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGVGSKCKGHPKAPKMPCAEDYLSVNLQNLVLEHKTTPVSDRVTKCTTES 480
Db 421 PTLVEVSRNLGVGSKCKGHPKAPKMPCAEDYLSVNLQNLVLEHKTTPVSDRVTKCTTES 480
Qy 481 LVNRRPCFSALEVDYTPKFNATFTFHADICTLSEKERQIKQOTALVELVVKHKPKAT 540
Db 481 LVNRRPCFSALEVDYTPKFNATFTFHADICTLSEKERQIKQOTALVELVVKHKPKAT 540
Qy 541 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
Db 541 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585

RESULT 12
US-10-413-831-1
; Sequence 1, Application US/10413831
; Publication No. US20030194813A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or M.D., David
; APPLICANT: Lau Ph.D., Edward
; APPLICANT: Winkler M.D., James V.
; TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
; TITLE OF INVENTION: Kits
; FILE REFERENCE: ISC007
; CURRENT APPLICATION NUMBER: US/10/413,831
; CURRENT FILING DATE: 2003-04-15
```

```
; PRIOR APPLICATION NUMBER: US/09/806,247
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/115,392
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: 60/102,738
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,926
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/165,581
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-413-831-1

Query Match      100.0%; Score 3103; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGGEENFKALVLJAFAPQYLQOCPPFEDHVKLVNEVTEFAKTCVADSEAE 60
Db 1 DAHKSEVAHRFKDLGGEENFKALVLJAFAPQYLQOCPPFEDHVKLVNEVTEFAKTCVADSEAE 60
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDQNPRLPLVRPEV 120
Db 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDQNPRLPLVRPEV 120
Qy 121 DVMTAFHNDNEETFLKYLVEIARRHPFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Db 121 DVMTAFHNDNEETFLKYLVEIARRHPFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
Qy 181 KLDELDRSGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVDLT 240
Db 181 KLDELDRSGKASSAKQRLKCSLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVDLT 240
Qy 241 VHTCCGDLLECCADRADLAKYICENQDS:SSKLKECCCKPFLLEKSHCIAEVENDEMPA 300
Db 241 VHTCCGDLLECCADRADLAKYICENQDS:SSKLKECCCKPFLLEKSHCIAEVENDEMPA 300
Qy 301 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEVYARRHPDYSVLLRLAKTYETLEKC 360
Db 301 DLPSLAADFVESKDVCKNVAEAKDVLGMFLYEVYARRHPDYSVLLRLAKTYETLEKC 360
Qy 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
Db 361 CAAADPHECYAKVDFEFKPLVEEPQNLIKONCELFQOLGEYKFNALLVRYTKKVPQVST 420
Qy 421 PTLVEVSRNLGVGSKCKGHPKAPKMPCAEDYLSVNLQNLVLEHKTTPVSDRVTKCTTES 480
Db 421 PTLVEVSRNLGVGSKCKGHPKAPKMPCAEDYLSVNLQNLVLEHKTTPVSDRVTKCTTES 480
Qy 481 LVNRRPCFSALEVDYTPKFNATFTFHADICTLSEKERQIKQOTALVELVVKHKPKAT 540
Db 481 LVNRRPCFSALEVDYTPKFNATFTFHADICTLSEKERQIKQOTALVELVVKHKPKAT 540
Qy 541 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585
Db 541 KEQLKAVMDDFAAFVEKCKKADDKETCFABEGKKLVAASQAALGL 585

RESULT 13
US-10-413-831-2
; Sequence 2, Application US/10413831
; Publication No. US20030194813A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or M.D., David
; APPLICANT: Lau Ph.D., Edward
; APPLICANT: Winkler M.D., James V.
; TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
; TITLE OF INVENTION: Kits
```

; FILE REFERENCE: ISCO07
 ; CURRENT APPLICATION NUMBER: US/10/413,831
 ; CURRENT FILING DATE: 2003-04-15
 ; PRIOR APPLICATION NUMBER: US/09/806,247
 ; PRIOR FILING DATE: 2001-07-16
 ; PRIOR FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: 60/115,392
 ; PRIOR FILING DATE: 1999-01-11
 ; PRIOR APPLICATION NUMBER: 60/102,738
 ; PRIOR FILING DATE: 1998-10-02
 ; PRIOR APPLICATION NUMBER: 09/165,926
 ; PRIOR FILING DATE: 1998-10-02
 ; PRIOR APPLICATION NUMBER: 09/165,581
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 585
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (1)-(585)
 ; OTHER INFORMATION: ACETYLATION
 ; US-10-413-831-2

Query Match 100.0%; Score 3103; DB 12; Length 585;
 Best Local Similarity 100.0%; Pred. No. 2.4e-269;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDGLGEENFKALVLIATAQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHRFKDGLGEENFKALVLIATAQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDNDPNLPLRVREPV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDNDPNLPLRVREPV 120
 QY 121 DVNCTAFHNEETFLKKLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 DB 121 DVNCTAFHNEETFLKKLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWARLSQRPFAEFAEVSCLVTDLT 240
 DB 181 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWARLSQRPFAEFAEVSCLVTDLT 240
 QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPFAEFAEVSCLVTDLT 300
 DB 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPFAEFAEVSCLVTDLT 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLVEYARRHPDYVSWLLRLAKTYETTLK 360
 DB 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLVEYARRHPDYVSWLLRLAKTYETTLK 360
 QY 361 CAAADPHECYAKVDFDFKPLVEEPQNLIKONCELPOLGEYKFNALLVRYTKVPQVST 420
 DB 361 CAAADPHECYAKVDFDFKPLVEEPQNLIKONCELPOLGEYKFNALLVRYTKVPQVST 420
 QY 421 PTLVEYSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTTCCTES 480
 DB 421 PTLVEYSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTTCCTES 480
 QY 481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTAALVELVVKHKPKAT 540
 DB 481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTAALVELVVKHKPKAT 540
 QY 541 KEQLKAVMDFFAAVFEKCKCKADDDKTCFAEEGKLVAAASQAALGL 585
 DB 541 KEQLKAVMDFFAAVFEKCKCKADDDKTCFAEEGKLVAAASQAALGL 585

RESULT 14
 US-10-153-064-5
 ; Sequence 5, Application US/10153064

; Publication No. US20020142814A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bell et al.
 ; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
 ; FILE REFERENCE: PF556
 ; CURRENT APPLICATION NUMBER: US/10/153,064
 ; CURRENT FILING DATE: 2002-05-24
 ; PRIOR APPLICATION NUMBER: 60/293,212
 ; PRIOR FILING DATE: 2003-05-25
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 585
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-10-153-064-5

Query Match 100.0%; Score 3103; DB 14; Length 585;
 Best Local Similarity 100.0%; Pred. No. 2.4e-269;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDGLGEENFKALVLIATAQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60
 DB 1 DAHSEVAHRFKDGLGEENFKALVLIATAQYLOQCPEDHVKLVNEVTEFAKTCVADESAAE 60
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDNDPNLPLRVREPV 120
 DB 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQPERNECFLOHKDNDPNLPLRVREPV 120
 QY 121 DVNCTAFHNEETFLKKLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 DB 121 DVNCTAFHNEETFLKKLYEIARRHPYFYAPPELLFFAKRYKAAFTTECCQAADKAACLLP 180
 QY 181 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWARLSQRPFAEFAEVSCLVTDLT 240
 DB 181 KLDELDEGKASSAKORLKCASLQKFGERAFAKAWARLSQRPFAEFAEVSCLVTDLT 240
 QY 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPFAEFAEVSCLVTDLT 300
 DB 241 VHTCCGDLLECCADRADLAKYICENQDSISSKLECCCKPFAEFAEVSCLVTDLT 300
 QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLVEYARRHPDYVSWLLRLAKTYETTLK 360
 DB 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLVEYARRHPDYVSWLLRLAKTYETTLK 360
 QY 361 CAAADPHECYAKVDFDFKPLVEEPQNLIKONCELPOLGEYKFNALLVRYTKVPQVST 420
 DB 361 CAAADPHECYAKVDFDFKPLVEEPQNLIKONCELPOLGEYKFNALLVRYTKVPQVST 420
 QY 421 PTLVEYSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTTCCTES 480
 DB 421 PTLVEYSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTTCCTES 480
 QY 481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTAALVELVVKHKPKAT 540
 DB 481 LVNRRPCFSALEVDYTVPKFNAETFTFHADICTLSEKERQIKKQTAALVELVVKHKPKAT 540
 QY 541 KEQLKAVMDFFAAVFEKCKCKADDDKTCFAEEGKLVAAASQAALGL 585
 DB 541 KEQLKAVMDFFAAVFEKCKCKADDDKTCFAEEGKLVAAASQAALGL 585

RESULT 15
 US-09-984-010-7
 ; Sequence 7, Application US/09984010
 ; Publication No. US20030104578A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ballance, David James
 ; TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
 ; AND SERUM ALBUMIN
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP

STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
MEDIUM TYPE: F-opy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent: Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,010
FILING DATE: 21-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,873
FILING DATE: 25-JUN-1998
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 19-DEC-1996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-984-010-7

Search completed: October 27, 2003, 15:17:09
Job time : 75 secs

Query Match 100.0%; Score 3103; DB 11; Length 604;
Best Local Similarity 100.0%; Pred. No. 2.5e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DAHSEVNAHREKDLGEENFKALVLIATAQYLCQPPFEDHVKLVNEVTEPAKTCVADESAE	60
Db	20	DAHSEVNAHREKDLGEENFKALVLIATAQYLCQPPFEDHVKLVNEVTEPAKTCVADESAE	79
Qy	61	NCDSLSLHTFGCKLCTVATLRETGEMADCCAKPEPERNECFLOHKDNPMLPRLVRPEV	120
Db	80	NCDSLSLHTFGCKLCTVATLRETGEMADCCAKPEPERNECFLOHKDNPMLPRLVRPEV	139
Qy	121	DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP	180
Db	140	DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP	199
Qy	181	KLDELDEGKASSAKQRLKCAASLOKFGSERAKAWAVARLSORFPKAEFAEVSKLVTDLTK	240
Db	200	KLDELDEGKASSAKQRLKCAASLOKFGSERAKAWAVARLSORFPKAEFAEVSKLVTDLTK	259
Qy	241	VHTECHGDLLECDRADLAKYICENQDSISSKKECCXPKLLEKSHCIAEVENDEMPA	300
Db	260	VHTECHGDLLECDRADLAKYICENQDSISSKKECCXPKLLEKSHCIAEVENDEMPA	319
Qy	301	DLPSLAADFVESKQVCKNYAEAKVFLGMFLYEVARRHPDYSVVLRLAKTYETTLTKC	360
Db	320	DLPSLAADFVESKQVCKNYAEAKVFLGMFLYEVARRHPDYSVVLRLAKTYETTLTKC	379
Qy	361	CAAADPHCEYAKVDFEPFLVPEEPONLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST	420
Db	380	CAAADPHCEYAKVDFEPFLVPEEPONLIKQNCLEFQELGEYKFNALLVRYTKKVPQVST	439
Qy	421	PTLVEVSNLKGKSKCKHPKAEKMPCAEDYLSVLNQLCVLHEKTPVSDRVTCKCTES	480
Db	440	PTLVEVSNLKGKSKCKHPKAEKMPCAEDYLSVLNQLCVLHEKTPVSDRVTCKCTES	499
Qy	481	LVNRRPCFSALEVDETYVPKEFNATFTFHADICTLSEKERQIKKQTALVELVXHKPKAT	540
Db	500	LVNRRPCFSALEVDETYVPKEFNATFTFHADICTLSEKERQIKKQTALVELVXHKPKAT	559
Qy	541	KEQLKAVMDDFAAVFVEKCKKADDDKETCFABEGKKLVAAASQAALGL	585
Db	560	KEQLKAVMDDFAAVFVEKCKKADDDKETCFABEGKKLVAAASQAALGL	604

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2003, 15:02:02 ; Search time 43 Seconds

(without alignments)
1308.341 Million cell updates/sec

Title: US-09-832-501-18

Perfect score: 3103

Sequence: 1 DAHKSVAHFKDLGEENFK.....TCFAEEGKLVAAQAALGL 585

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3103	100.0	609	1 ABHUS	serum albumin prec
2	2942	94.8	602	2 A47391	serum albumin prec
3	2620	84.4	608	2 S57632	serum albumin prec
4	2475.5	79.8	607	1 ABHOS	serum albumin prec
5	2446.5	78.8	607	1 ABHOS	serum albumin prec
6	2432.5	78.4	607	1 ABHOS	serum albumin prec
7	2426	78.2	608	1 ABR7S	serum albumin prec
8	2411.5	77.7	605	1 ABPGS	serum albumin prec
9	2387	76.9	609	2 JCS838	albumin - Mongolia
10	1864	60.0	453	2 A05139	serum albumin - mo
11	1557.5	50.2	615	1 ABCHS	serum albumin prec
12	1253.5	40.4	609	2 JCA258	alpha-fetoprotein
13	1249.5	40.3	609	1 PPHU	alpha-fetoprotein
14	1242.5	40.0	609	1 PPGO	alpha-fetoprotein
15	1205	38.8	607	1 ABXL72	74K albumin prec
16	1181.5	38.1	285	2 I46986	albumin - dog (fra
17	1175.5	37.9	608	1 ABX168	68K serum albumin
18	1084	34.9	605	1 FPMS	alpha-fetoprotein
19	1067	34.4	611	1 FPRT	alpha-fetoprotein
20	1055	34.0	599	1 A54906	afamin precursor -
21	928.5	29.9	614	2 S59517	serum albumin prec
22	928	29.9	608	2 A53195	afamin precursor -
23	747.5	24.1	608	1 ABONS1	serum albumin 1 pr
24	742.5	23.9	608	1 ABONS2	serum albumin 2 pr
25	699	22.5	382	2 A37253	serum albumin - bu
26	440.5	14.2	1423	1 S27941	serum albumin - se
27	386	12.4	474	1 VYHDD	vitamin D-binding
28	385	12.4	476	1 VYRTD	vitamin D-binding
29	372	12.0	472	1 A35327	vitamin D-binding

30 184 5.9 181.9 2 A71928
31 184 5.9 192.7 2 G64585
32 141.5 4.6 1560 2 T30282
33 137.5 4.4 1348 2 AG2558
34 134.5 4.3 1004 2 JC2221
35 134 4.3 1083 2 JC2300
36 134 4.3 1780 2 T17272
37 133.5 4.3 1390 2 S51364
38 132.5 4.3 1070 2 T06733
39 131 4.2 1076 2 JC2217
40 130 4.2 1175 2 D35815
41 129 4.2 1017 2 JC4035
42 128.5 4.1 1051 2 JC4091
43 128 4.1 1005 2 A64465
44 128 4.1 3225 2 I52300
45 126.5 4.1 1927 2 A59236

cag island protein
cag pathogenicity
calcium-binding pr
hypothetical prote
major surface glyco
cell surface glyco
hypothetical prote
hypothetical prote
sperm tail-specifi
kinesin homolog P2
major surface glyco
myosin heavy chain
cell-cycle-depende
glycoprotein A - P
hypothetical prote
giantin - human
embryonic muscle m

ALIGNMENTS

RESULT 1

ABHUS
serum albumin precursor [validated] - human
N:Alternate names: preproalbumin
N:Contains: Kinetensin
C:Species: Homo sapiens (man)
C>Date: 29-Jul-1991 #sequence revision 31-Jan-1997 #text change 17-Mar-2000
C:Accession: A93743; A93936; I39427; I59286; I39427; G01747; S55314; A91420; S06422; ;
R:Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; See
Nucleic Acids Res. 9, 6103-6114, 1981
A:Title: The sequence of human serum albumin cDNA and its expression in Escherichia co
A:Reference number: A93743; MUID:82081882; PMID:6171778
A:Accession: A93743
A:Molecule type: mRNA
A:Residues: 1-419; 'K', 421-609 <LAW>
A:Cross-references: EMBL:V00495; GB:J00078; GB:LC0132; GB:LC0133; NID:G28591; PIDN:CAJ
R:Dugaiczky, A.; Law, S.W.; Dennison, O.E.
Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982
A:Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.
A:Reference number: A93936; MUID:82105994; PMID:6275391
A:Accession: A93936
A:Molecule type: mRNA
A:Residues: 1-120; 'G', 122-609 <DUG>
A:Cross-references: EMBL:V00494; NID:G28589; PIDN:CAA23753.1; PID:G28590
R:Ueno, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.
J. Biol. Chem. 261, 3244-3251, 1986
A:Title: The human albumin gene. Characterization of the 5' and 3' flanking regions at
A:Reference number: I39427; MUID:86140099; PMID:2419329
A:Accession: I39427
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-26 <URA>
A:Cross-references: GB:W13075; NID:G178330; PIDN:AAAS1688.1; PID:G553173
R:Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994
A:Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fami
A:Reference number: I59286; MUID:94181575; PMID:8134387
A:Accession: I59286
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 282-290; 'KSRFDLQ' <WAT>
A:Cross-references: GB:S69192; NID:G546032; PIDN:AAB30282.1; PID:G546033
A>Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia
R:Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putnar
Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994
A:Title: Genetic variants of human serum albumin in Italy: point mutants and a carboxy
A:Reference number: I59313; MUID:94294404; PMID:8022807
A:Accession: I59313
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 589-590; 'ALPRVRNLLQVKLP' <NAD>
A:Cross-references: GB:S70799; NID:G547231; PIDN:AAB31177.1; PID:G547232

A:Note: this frame-shift variant is designated albumin Bazzano; four additional variants
 R:Menava, J.; Parrilla, R.; Ayuso, M.S.
 Submitted to the EMBL Data Library, March 1995
 A:Reference number: G08292
 A:Accession: G01747
 A:Status: translated from GB/EMSL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-120, 'G', 122-455 <MEN>
 A:Cross-references: EMBL:U02961; MID:9763428; PIDN:AAA64922.1; PID:9763431
 R:Ledgerwood, E.C.; George, P.W.; Peach, R.O.; Brennan, S.O.
 Biochem. J. 308, 321-325, 1995
 A:Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast *Kex2*
 A:Reference number: S55314; MID:95275251; PMID:7755581
 A:Accession: S55314
 A:Molecule type: protein
 A:Residues: 19-27 <LED>
 R:Meloun, B.; Moravek, L.; Kostka, V.
 FEBS Lett. 58, 134-137, 1975
 A:Title: Complete amino acid sequence of human serum albumin.
 A:Reference number: A91420; MID:76187907; PMID:1225573
 A:Accession: A91420
 A:Molecule type: protein
 A:Residues: 25-117, 'G', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-400
 R:Roehr, U.; Spittler, G.; Tripiet, D.
 Justus Liebig's Ann. Chem. 9, 881-884, 1988
 A:Title: Isolation and structure elucidation of middle-molecular weight peptides from urine
 A:Reference number: S06422
 A:Note: this paper is in German, with an English abstract
 A:Accession: S06422
 A:Molecule type: protein
 A:Residues: 25-48 <ROE>
 R:Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
 Arch. Biochem. Biophys. 305, 595-599, 1993
 A:Title: Mass spectrometric identification of modifications to human serum albumin treated with hydrogen peroxide
 A:Reference number: S36882; MID:93384321; PMID:8373198
 A:Accession: S36882
 A:Molecule type: protein
 A:Residues: 45-67, 141-160, 311-337, 469-490, 570-581 <FIN>
 R:Kausler, E.; Spittler, G.
 Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
 A:Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmolekule
 A:Reference number: S17599; MID:92126241; PMID:1772598
 A:Accession: S17599
 A:Molecule type: protein
 A:Residues: 25-54, 354-357, 431-447 <KAU>
 A:Note: 49-Leu was also found
 R:Caraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
 J. Immunol. 143, 1680-1684, 1989
 A:Title: Structures of histamine-releasing peptides formed by the action of acid proteases
 A:Reference number: A45800; MID:89341406; PMID:2474609
 A:Accession: A45800
 A:Molecule type: protein
 A:Residues: 166-173, 'L' <CAR>
 R:Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, C.E.; Ward, J.
 Biochem. Biophys. Res. Commun. 136, 983-988, 1986
 A:Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-treated porcine stomach mucosa
 A:Reference number: A03239; MID:86242180; PMID:3087352
 A:Accession: A03239
 A:Molecule type: protein
 A:Residues: 166-173, 'L' <MOG>
 R:Galliano, M.; Minichotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
 A:Title: Mutations in genetic variants of human serum albumin found in Italy.
 A:Reference number: A38255; MID:91062352; PMID:2247440
 A:Accession: A38255
 A:Molecule type: protein
 A:Residues: 76-111 <GAL1>
 A:Accession: B38255
 A:Molecule type: protein
 A:Residues: 82-105, 'K', 107-110 <GAL2>
 A:Note: this variant is designated albumin Vibo Valentia
 A:Accession: A38255
 A:Molecule type: protein

A:Residues: 76-83, 'K', 85-106 <GAL3>
 A:Note: this variant is designated albumin Torino
 R:Minichotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
 Eur. J. Biochem. 214, 437-444, 1993
 A:Title: The structural characterization and bilirubin-binding properties of albumin
 A:Reference number: S33298; MID:93292504; PMID:8513793
 A:Accession: S33298
 A:Molecule type: protein
 A:Residues: 255-263, 'E', 265-281 <MIN1>
 A:Note: this variant is designated albumin Herborn
 R:Minichotti, L.; Galliano, M.; Scoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Porzio, B.
 Biochim. Biophys. Acta 1119, 232-238, 1992
 A:Title: Two albumins with identical electrophoretic mobility are produced by different genes
 A:Reference number: S21078; MID:92190239; PMID:11347703
 A:Accession: S21078
 A:Molecule type: protein
 A:Residues: 354-356, 'K', 358-378 <MIN2>
 A:Note: this variant is designated albumin Sondrio; another variant Paris-2 is reported
 R:He, X.M.; Carter, D.C.
 Nature 358, 209-215, 1992
 A:Title: Atomic structure and chemistry of human serum albumin.
 A:Reference number: A46756; MID:92334427; PMID:1630489
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms
 R:Brown, J.R.; Shockley, P.; Behrens, P.O.
 In The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp.23-33
 A:Reference number: A94442
 A:Contents: annotation; three-dimensional structure and disulfide bonds
 R:Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
 Collect. Czech. Chem. Commun. 42, 564-579, 1977
 A:Title: Disulfide bonds in human serum albumin.
 A:Reference number: A90930
 A:Contents: annotation; disulfide bonds
 R:Jacobsen, C.
 Biochem. J. 171, 453-459, 1978
 A:Title: Lysine residue 240 of human serum albumin is involved in high-affinity binding of bilirubin
 A:Reference number: A90299; MID:78186630; PMID:656055
 A:Contents: annotation; bilirubin-binding site
 R:Peterson, T.; Reed, R.G.
 In Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjöholm, I., eds., 11-15
 A:Title: Serum albumin: conformation and active sites.
 A:Reference number: A94408
 A:Contents: annotation; binding sites
 R:Harper, M.E.; Dugaiczky, A.
 Am. J. Hum. Genet. 35, 565-572, 1983
 A:Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein genes
 A:Reference number: A90028; MID:83279982; PMID:6192711
 A:Contents: annotation; gene position
 R:Walker, J.E.
 FEBS Lett. 66, 173-175, 1976
 A:Title: Lysine residue 199 of human serum albumin is modified by acetylsalicylic acid
 A:Reference number: A46755; MID:76257808; PMID:955075
 A:Contents: annotation
 A:Note: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicylic acid) to lysine residue 199 of human serum albumin
 R:Bohney, J.P.; Fonda, M.L.; Feldhoff, R.C.
 FEBS Lett. 298, 266-268, 1992
 A:Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phosphate
 A:Reference number: A56294; MID:92183881; PMID:1544460
 A:Contents: annotation
 A:Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; it is a catalytic activity
 A:Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized in the liver, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (we have not found any other variants of human serum albumin have been described).
 C:Genetics:
 A:Gene: GDB:ALB
 A:Cross-references: GDB:118990; OMIM:103600
 A:Map position: 4q11-q13
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyridoxal 5'-phosphate
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-609/Product: serum albumin #status experimental <MPT>
 F:29-202/Domain: serum albumin repeat homology <SA1>

F:166-174/Product: kinetensin #status experimental <KIP>
F:221-394/Domain: serum albumin repeat homology <SA2>
F:413-592/Domain: serum albumin repeat homology <SA2>
F:27/Binding site: copper (His) #status predicted
F:77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-3-3,340-385,384-393,4
F:214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 100.0%; Score 3103; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 9, 2e-198;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFDGLGENFALVLIAPAOYLQOCPFEDHVKLVNEVTEFAKTCVADESAE 60
DB 25 DAHSEVAHRFDGLGENFALVLIAPAOYLQOCPFEDHVKLVNEVTEFAKTCVADESAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 144
QY 121 DVNCTAFHDNEETFLKKLYLVEIARRHPYFYAPELLFFAKRYKAAAFTECCQAADKAACLLP 180
DB 145 DVNCTAFHDNEETFLKKLYLVEIARRHPYFYAPELLFFAKRYKAAAFTECCQAADKAACLLP 204
QY 181 KLDELDEGKASSAKORLKASLQKFGERAFAKAWAVARLSORFPKAFPAEVSKLVTDLTK 240
DB 205 KLDELDEGKASSAKORLKASLQKFGERAFAKAWAVARLSORFPKAFPAEVSKLVTDLTK 264
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKECCCKPILLESKSHGIAEVENDEMPA 300
DB 265 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKECCCKPILLESKSHGIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYVSVLLRLRAKYETTTLEKC 360
DB 325 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYVSVLLRLRAKYETTTLEKC 384
QY 361 CAAADPHECYAKVDFBFPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
DB 385 CAAADPHECYAKVDFBFPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 444
QY 421 PTLVEVSRNLGKVGSKCCCKHPKAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEVSRNLGKVGSKCCCKHPKAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 504
QY 481 LVNRRPCFSALEVDYTPVPEKFAEVECKADDKETCFABEGKKLVAASQAALG 540
DB 505 LVNRRPCFSALEVDYTPVPEKFAEVECKADDKETCFABEGKKLVAASQAALG 564

RESULT 2
A47391
serum albumin precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #ext_change 20-Aug-1999
C:Accession: A47391
R:Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwyer, J.; Putnam, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
A:Title: cDNA and protein sequence of polymorphic macaque albumins that differ in bilirubin binding site
A:Reference number: A47391; MUID:93211971; PMID:8460152
A:Contents: B/B homozygote
A:Accession: A47391
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-600 <WAT>
A:Cross-references: GB:M90463; NID:G342294; PIDN:AAA36906.1; PID:G342295
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBI:128280, NCBI:128281)
C:Superfamily: serum albumin; serum albumin repeat homology
F:21-194/Domain: serum albumin repeat homology <SA1>
F:213-386/Domain: serum albumin repeat homology <SA2>

F:405-584/Domain: serum albumin repeat homology <SA3>
Query Match 94.8%; Score 2942; DB 2; Length 600;
Best Local Similarity 93.5%; Pred. No. 4e-187;
Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 1 DAHSEVAHRFDGLGENFALVLIAPAOYLQOCPFEDHVKLVNEVTEFAKTCVADESAE 60
DB 17 DTHSEVAHRFDGLGEEHFKGLVLPVAFSQYLOQCPFEEHVKLVNEVTEFAKTCVADESAE 76
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 120
DB 77 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEV 136
QY 121 DVNCTAFHDNEETFLKKLYLVEIARRHPYFYAPELLFFAKRYKAAAFTECCQAADKAACLLP 180
DB 137 DVNCTAFHDNEETFLKKLYLVEIARRHPYFYAPELLFFAKRYKAAAFTECCQAADKAACLLP 196
QY 181 KLDELDEGKASSAKORLKASLQKFGERAFAKAWAVARLSORFPKAFPAEVSKLVTDLTK 240
DB 197 KLDELDEGKASSAKORLKASLQKFGERAFAKAWAVARLSORFPKAFPAEVSKLVTDLTK 256
QY 241 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKECCCKPILLESKSHGIAEVENDEMPA 300
DB 257 VHTCCCHGDLLECCADRADLAKYICENQDSISSKLKECCCKPILLESKSHGIAEVENDEMPA 316
QY 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYVSVLLRLRAKYETTTLEKC 360
DB 317 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYFYARRHPDYVSVLLRLRAKYETTTLEKC 376
QY 361 CAAADPHECYAKVDFBFPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 420
DB 377 CAAADPHECYAKVDFBFPLVEEPQNLIKQNCLEFQOLGEYKFNALLVRYTKKVPQVST 436
QY 421 PTLVEVSRNLGKVGSKCCCKHPKAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 437 PTLVEVSRNLGKVGSKCCCKHPKAKMPCAEADYLSVLNQLCVLHEKTPVSDRVTKCCTES 496
QY 481 LVNRRPCFSALEVDYTPVPEKFAEVECKADDKETCFABEGKKLVAASQAAL 540
DB 497 LVNRRPCFSALEVDYTPVPEKFAEVECKADDKETCFABEGKKLVAASQAAL 556
QY 541 KEQLKAVMDPFAAFVEKCKADDKETCFABEGKKLVAASQAAL 583
DB 557 KEQLKAVMDPFAAFVEKCKADDKETCFABEGKKLVAASQAAL 599

RESULT 3
S57632
serum albumin precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #ext_change 20-Aug-1999
C:Accession: J04660; S57632
R:Hilger, C.; Grigioni, F.; Hentges, F.
Gene 169, 235-296, 1996
A:Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A:Reference number: J04660; MUID:96194824; PMID:8647469
A:Accession: J04660
A:Molecule type: mRNA
A:Residues: 1-608 <H12>
A:Cross-references: EMBL:X84842; NID:G886484; PIDN:CAA59279.1; PID:G886485
A:Experimental source: liver
A:Comment: This protein is the major protein component in plasma. It functions as a m
ein has 35 conserved cysteine residues.
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: liver; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PP>
F:25-608/Product: serum albumin #status predicted <MAT>
F:229-202/Domain: serum albumin repeat homology <SA1>
F:221-394/Domain: serum albumin repeat homology <SA2>
F:413-592/Domain: serum albumin repeat homology <SA3>

Query Match 84.4%; Score 2620; DB 2; Length 608;
Best Local Similarity 82.0%; Pred. No. 8.2e-166;
Matches 478; Conservative 52; Mismatches 53; Indels 0; Gaps 0;

QY 1 DAHSEVAHRRFKDGBENFKALVLIAPAYVQOCPPFEDHVKLVNEVTEFAKTCVADESSE 60
DB 25 EAHQSEIAHRRFNDLGEHFFGLVLVAFSQYLOQCPFEDHVKLVNEVTEFAKGCVAQDSAA 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVLRPEV 120
DB 85 NCKSLHLLGCKLCTVASURDKYGENADCCCKEPERNECFLOHKDDNPGLVTPRA 144
QY 121 DVMTAFPHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKYKAAFTTECCOAAADKAACLIP 180
DB 145 DAMCTAFHENEQRFGLKYLVEIARRHPYFYAPPELLFYAEYKGVFTCECAADKAACLIP 204
QY 181 KLDELREGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 205 KVDALREKVLASSAKERLKASLQKGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 264
QY 241 VHTCECHGDLLECCADDRADLAKYICENQDSISSKLKECCCKPFLLEKSHCIAEVENDEMPA 300
DB 265 IHKECCGDLLECCADDRADLAKYICENQDSISSKLKECCCKPFLLEKSHCIAEVENDEMPA 324
QY 301 DLPSLAADFVESKDVCKVYAEAKDVFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEKC 360
DB 325 DLPLAVDFVEDKVCVCKVYAEAKDVFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEKC 394
QY 361 CAADAPHECYAKVDFEPKPLVEEPONLIKONCELFEOLOGYKFNALLVRYTKKYPQVST 420
DB 385 CATDDPACVAVHDFEPKPLVEEPONLIKONCELFEOLOGYKFNALLVRYTKKYPQVST 444
QY 421 PTLVEVSRNLGKVGSKCKPKEAKRMPCAEDYSVLNQLCVLHEKTPVSDRVTKCTES 480
DB 445 PTLVEVSRNLGKVGSKCKPKEAKRMPCAEDYSVLNQLCVLHEKTPVSDRVTKCTES 504
QY 481 LVNRRPCFSALEVDYVYKPFNAETFTFHADICTLSEKERQIKQOTALVELVKKPKAT 540
DB 505 LVNRRPCFSALEVDYVYKPFNAETFTFHADICTLSEKERQIKQOTALVELVKKPKAT 564
QY 541 KEQLKAVMDDFAAFEVCKCKADKDETCFAEKGKLVAAASQAL 583
DB 565 BEQLKTVMGDFGFSVDKCAAEKDEACFAEKGKLVAAASQAL 607

RESULT 4

ABHOS
serum albumin precursor - horse
C:Species: Equus caballus (domestic horse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: S34053
R:Ho, J. X.; Holowachuk, E. W.; Norton, E. J.; Twigg, P. D.; Carter, D. C.
Eur. J. Biochem. 215, 205-212, 1993
A:Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
A:Reference number: S34053; MUID:93345495; PMID:8344282
A:Accession: S34053
A:Molecule type: mRNA
A:Residues: 1-607 <HOA>
A:Cross-references: GB:X74045; NID:G9399671; PIDN:CAA52194.1; PID:G9399672
A:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membrane).
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:118/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-Product: serum albumin #status predicted <VAT>
F:29-201/Domain: serum albumin repeat homology <SA1>
F:220-393/Domain: serum albumin repeat homology <SA2>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:27/Binding site: copper (His) #status predicted
F:77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,400-401/Binding site: bilirubin (Lys) #status predicted

Query Match 79.8%; Score 2475.5; DB 1; Length 607;
Best Local Similarity 76.3%; Pred. No. 3e-156;
Matches 445; Conservative 69; Mismatches 68; Indels 1; Gaps 1;

QY 1 DAHSEVAHRRFKDGBENFKALVLIAPAYVQOCPPFEDHVKLVNEVTEFAKTCVADESSE 60
DB 25 DTHKSEIAHRRFNDLGEHFFGLVLVAFSQYLOQCPFEDHVKLVNEVTEFAKCAADESSE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVLRPEV 120
DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPRLVLRPEV 143
QY 121 DVMTAFPHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKYKAAFTTECCOAAADKAACLIP 180
DB 144 DAQCAAFQEDPKFLGKYLVEVARRHPYFYAPPELLFFAEYKADFTTECCPADDLKACLIP 203
QY 181 KLDELREGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 240
DB 204 KLDELREGKASSAKQRLKASLQKGERAFKAWAVARLSQRPKAEFAEVSKLVTDLTK 263
QY 241 VHTCECHGDLLECCADDRADLAKYICENQDSISSKLKECCCKPFLLEKSHCIAEVENDEMPA 300
DB 264 VHTCECHGDLLECCADDRADLAKYICENQDSISSKLKECCCKPFLLEKSHCIAEVENDEMPA 323
QY 301 DLPSLAADFVESKDVCKVYAEAKDVFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEKC 360
DB 324 DLPSLAADFVESKDVCKVYAEAKDVFLGMFLYFYARRHPDYVSVLLRLAKTYETTTLEKC 383
QY 361 CAADAPHECYAKVDFEPKPLVEEPONLIKONCELFEOLOGYKFNALLVRYTKKYPQVST 420
DB 384 CAADAPHECYAKVDFEPKPLVEEPONLIKONCELFEOLOGYKFNALLVRYTKKYPQVST 443
QY 421 PTLVEVSRNLGKVGSKCKPKEAKRMPCAEDYSVLNQLCVLHEKTPVSDRVTKCTES 480
DB 444 PTLVEVSRNLGKVGSKCKPKEAKRMPCAEDYSVLNQLCVLHEKTPVSDRVTKCTES 503
QY 481 LVNRRPCFSALEVDYVYKPFNAETFTFHADICTLSEKERQIKQOTALVELVKKPKAT 540
DB 504 LVNRRPCFSALEVDYVYKPFNAETFTFHADICTLSEKERQIKQOTALVELVKKPKAT 563
QY 541 KEQLKAVMDDFAAFEVCKCKADKDETCFAEKGKLVAAASQAL 583
DB 564 KEQLKAVMDDFAAFEVCKCKADKDETCFAEKGKLVAAASQAL 606

RESULT 5
ABHOS
serum albumin precursor [validated] - bovine
N:Alternate names: 67K protein; preproalbumin
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: A38885; A36401; A91258; B60808; S10780; D45800; A26693; A90309; A91458;
R:Holowachuk, E. W.; Stoltzenberg, J. K.; Reed, R. G.; Peters Jr., T.
Submitted to the EMBL Data Library, August 1991
A:Description: Bovine serum albumin: cDNA sequence and expression.
A:Reference number: A38885
A:Accession: A38885
A:Molecule type: mRNA
A:Residues: 1-607 <HOL>
A:Cross-references: EMBL:M73215
R:Hiyama, K.; Akashi, S.; Furuya, M.; Fukuhara, K.
Biochem. Biophys. Res. Commun. 173, 639-646, 1990
A:Title: Rapid confirmation and revision of the primary structure of bovine serum alt
A:Reference number: A36401; MUID:91083649; PMID:2260975
A:Accession: A36401
A:Molecule type: protein
A:Residues: 25-41, 'H', 43-189, 'E', 191-213, 'T', 215-323, 'D', 325-393, 'TS', 396-607 <HIR>
R:MacGillivray, R. T. A.; Chung, D. W.; Davie, E. W.
Eur. J. Biochem. 98, 477-485, 1979
A:Title: Biosynthesis of bovine plasma proteins in a cell-free system.
A:Reference number: A91258; MUID:80024278; PMID:488109
A:Accession: A91258
A:Molecule type: protein

Query Match 78.8%; Score 2446.5; DB 1; Length 607;

```
Best Local Similarity   75.6%; Pred. No. 2.5e+154;
Matches 441; Conservative 71; Mismatches 70; Indels 1; Gaps 1;
```

Cy 1 DAKHSEVAHRFNDGDLGEENFKALVLIAPAYQLQQCPFFEDHVKLNVNEVFTEFAKTCVADESA 60
Db 25 DTHKEIAHRFNLDLGBEQFGVLVIAPSQYLQOCPFFDEHVKLNLNELTFEFAKTCVADSHA 84

Cy 61 NCKSLHTLFGBDKLTCTVALRTETYGENADCACAEPEERNECFLOHKDKNPNLPVLVRPEV 120
Db 85 GGEKSHTLTFGBELCKVASLRETYGDMADECCEQEPEERNECFLSHKDSDPLPKL-NPDP 143

Cy 121 DWMTAFHDNBSFTLKLYLYETARHPHYFYAPELLFFPAKYKAATFECCQAADKAACLLP 180
Db 144 NTLCDFEKADEKKFWGKLYLYETARHPHYFYAPELLYYANKYNGVFDQCCQAEKGCALLP 203

Cy 181 KDELRLDEKGASSAQRILKCASLQKFGERAPKAWAVARLSQRFPAKBAEVSCLKVTDTTK 240
Db 204 KIETMRKVLAASSAROLRCASIQKFGERALKWAVARLSQKFPKABRVEVTVTLVDLTK 263

Cy 241 VITECHGGDLLCACDRADRALIYCENODSISSKLKECCXPLEKSHCIAEVENDEMPA 300
Db 264 VHKECHGGDLLCACDRADRALIYICDNQDTSSKLKECCDXPLEKSHCIAEAEEKDAIPE 323

Cy 301 DLPSLAADFVESKDYCKNYAAKDVFLGMELYEARRHDPDYSVVLLRLAKTYETTLEKC 360
Db 324 NUPLTADPAEDKDYCKNYOEAKDAFLSGFLYESRRHPEYAVSVILLRAKEYEATILEEC 383

Cy 361 CAAAPDHBCYAKVPDEFKPLVEEPONLIKQCCELFEQLGEYKGFONALLVRYTKKVPQVST 420
Db 384 CARDDPHACYSTVFDKHLHEDPONLIKQCDOPFKLGEGYGFONALLYRVTRYKVPQVST 443

Cy 421 PTLVEVSRLNGVKVGSKCKKHBEAKMPCAEDVLSVVLNQGLVHLHEKTIVSPDRVTKCCTES 480
Db 444 PTLVEVSRSJGVKGTGRCTCKPESEMPTCEDYLSILNRCLVHLHEKTIVSEKVTVCCTES 503

Cy 481 LVNRRPCFSALEVDITYYPKFNASTFTFHADICTLSEKERQKKQTALVELVHXHKPKAT 540
Db 504 LVNRRPCFSALTPTYTPYKPAFDEKLTFHADICTLPOTEKQKKQTALVELLVXHKPKAT 563

Cy 541 KSQLKAVMDMDFAAFYEKKCKADDKETCFABEGKLVAAASAAL 583
Db 564 EQLQKTMVENVAFVDKCAAADREACFAVEGPKLWISTOTAL 606

RESULT 6
ABSHS
serum albumin precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: S06936
R:Brown, W.X.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A>Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A:Reference number: S06936; MUID: 90098888; PMID: 2602160
A:Accession: S06936
A:Molecule type: mRNA
A:Residues: 1-607 <BRO>
A:Cross-references: EMBL:X17055; NID:GI386; PID:CAA34903.1; PDB:gl387
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper-
tetrad hormones (weak bonds) with these hormones promote their transfer across the mem-
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-607/Product: serum albumin #status predicted <MAT>
F:29-201/Domain: serum albumin repeat homology <SA1>
F:220-393/Domain: serum albumin repeat homology <SA2>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:427/Binding site: copper (His) #status predicted
F:77-86,99-1-5,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-393;
F:263/Binding site: bilirubin (Lys) #status predicted

```
Best Local Similarity 75.0%; Pred. No. 2, 1e-153;
Matches 437; Conservative 73; Mismatches 72; Indels 1; Gaps 1;

QY 1 DAHKEVAHFRKDLGSENFKALVLIAFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
D 25 DTHKEIAHFRNDLGEENFQGSVLIAFSGYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDPNLPLVREPV 120
D 85 GCDKSLHTLFGDELCKVATLRETYGDMADCCBKQEPERNECFLOHKDNDPNLPLVREPV 143
QY 121 DVMCTAFHNDNEETFLKKLYEYARRHPHYFAPPELLFFAKRYKAAFTCCQADKAACLLP 180
D 144 DTLCAEFKADKFKFKYLYEVARHPHYFAPPELLFYANKYNGVFOEQCOAEDKGCALLP 203
QY 181 KLDELRDEGKASSAKRLKASLOKFGERAFKAWAVARLSQRFKAPFAEYSKLVITLTK 240
D 204 KIDAKREKVLASSAKQRLKASLOKFGERAFKAWAVARLSQRFKAPFAEYSKLVITLTK 263
QY 241 VHTCECHGDLLECADRADLAKYICENQDS:SSKLKECCEKPLLEKSHCAEVENDEMPA 300
D 264 VHKCECHGDLLECADRADLAKYICDHQDALSSKLKECCEKPLLEKSHCAEVENDEMPA 323
QY 301 DLPSLAADPVEKSKYKNAEAKDYFLGMFLYEAARRHPHYFAPPELLFFAKRYKAAFTCCQADKAACLLP 360
D 324 NLPLPTADPAEDKFKYKNAEAKDYFLGMFLYEAARRHPHYFAPPELLFFAKRYKAAFTCCQADKAACLLP 383
QY 361 CAAADPHECYAKVDFEFKPLVEEPONLJKONCELFPEQOLGEYKFNQALVRYTKKVPQVST 420
D 384 CAKEDPHACYATVDFKPLVDEPNLJKONCELFPEQOLGEYKFNQALVRYTKKVPQVST 443
QY 421 PTLVEVSRNLGVSKCKKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCTES 480
D 444 PTLVEISRLGVSKCKKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKCTES 503
QY 481 LVNRAPCFSALEVDETYVPKFNATFTFHADICTLSEKEROIKQOTALVELVGHKPKAT 540
D 504 LVNRAPCFSDLTLDCTYVPKFNATFTFHADICTLSEKEROIKQOTALVELVGHKPKAT 563
QY 541 KEOLKAVMDDEFAFVEKCKADKDKETCAEEGKGLVAASQAL 583
D 564 DEQLKTVNENFVAFVDDKCAADKCEGCFVLEGFKLVASTQAL 606

RESULT 7
ABRTS
serum albumin precursor - rat
N:Alternate names: preproalbumin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 22-Jun-1999
C:Accession: A93872; A92211; A91946; A91940; C45800; I57621; A03233
R:Sargent, T.D.; Yang, M.; Bonner, J.
Proc. Natl. Acad. Sci. U.S.A. 78, 243-246, 1981
A:Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A:Reference number: A93872; MUID:81223722; PMID:7017712
A:Accession: A93872
A:Molecule type: mRNA
A:Residues: 1-608 <SAR>
A:Cross-references: GB:V01222; GB:J00698; NID:G55627; PIDN:CAA24532.1; PID:G55628
R:Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
J. Biol. Chem. 252, 6846-6855, 1977
A:Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analysis
A:Reference number: A92211; MUID:77249657; PMID:893447
A>Note: Cleavages during protein maturation
A:Accession: A92211
A:Molecule type: protein
A:Residues: 1-38 <STR>
R:Isemura, S.; Ikenaka, T.
J. Biochem. 83, 35-48, 1978
A:Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
A:Reference number: A91946; MUID:78109429; PMID:564345
A:Accession: A91946
A:Molecule type: protein
```

```
A:Residues: 25-222 <ISI>
R:Isemura, S.; Ikenaka, T.
J. Biochem. 79, 1183-1196, 1976
A:Title: Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amin
A:Reference number: A91940; MUID:76260153; PMID:956149
A:Accession: A91940
A:Molecule type: protein
A:Residues: 223-288:572-608 <IS2>
A>Note: 262-Leu was also found
R:Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A:Title: Copper(III)-binding ability of human alpha-fetoprotein.
A:Reference number: A90758; MUID:79001617; PMID:80265
A:Contents: annotation; copper binding
R:Caraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1890-1898, 1989
A:Title: Structures of histamine-releasing peptides formed by the action of acid prot
A:Reference number: A45800; MUID:89341406; PMID:2474609
A:Accession: C45800
A:Status: preliminary
A:Molecule type: protein
A:Residues: 166-173 <CAR>
R:Heard, J.
Mol. Cell. Biol. 7, 2425-2434, 1987
A:Title: Determinants of rat albumin promoter tissue specificity analyzed by an impr
A:Reference number: I57621; MUID:87286876; PMID:3475566
A:Accession: I57621
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M16825; NID:G202828; PIDN:AAA40712.1; PID:G554412
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:1-18/Domain: signal sequence #status experimental <SIG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:25-608/Product: serum albumin #status experimental <MAT>
F:29-202/Domain: serum albumin repeat homology <SA1>
F:221-394/Domain: serum albumin repeat homology <SA2>
F:413-592/Domain: serum albumin repeat homology <SA3>
F:27/Binding site: copper (HIS) #status experimental
F:77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-385
Query Match 78.2%; Score 2426; DB 1; Length 608;
Best Local Similarity 73.4%; Pred. No. 5, 6e-153;
Matches 428; Conservative 82; Mismatches 73; Indels 0; Gaps 0;

QY 1 DAHKEVAHFRKDLGSENFKALVLIAFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 60
D 25 EAHKEIAHFRKDLGSENFKALVLIAFAQYLOQCFFEDHVKLVNEVTEFAKTCVADESAAE 84
QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDPNLPLVREPV 120
D 85 NCDKSLHTLFGDKLCAIPKLRDNYGELADCCAKQEPERNECFLOHKDNDPNLPLVREPV 144
QY 121 DVMCTAFHNDNEETFLKKLYEYARRHPHYFAPPELLFFAKRYKAAFTCCQADKAACLLP 180
D 145 EAMCTSFQENPTSLFLGHLHYEVARHPHYFAPPELLFYAEKYNELVTQCCTESDKAALTP 204
QY 181 KLDELRDEGKASSAKQRLKASLOKFGERAFKAWAVARLSQRFKAPFAEYSKLVITLTK 240
D 205 KLDVAVKEKALVAARVQRMKCSMQRFGERAFKAWAVARLSQRFKAPFAEYSKLVITLTK 264
QY 241 VHTCECHGDLLECADRADLAKYICENQDS:SSKLKECCEKPLLEKSHCAEVENDEMPA 300
D 265 INKECCHGDLLECADRADLAKYICENQATISLKLQACCDKPKLQSKQCLAEHEDNIPA 324
QY 301 DLPSLAADPVEKSKYKNAEAKDYFLGMFLYEAARRHPHYFAPPELLFFAKRYKAAFTCCQADKAACLLP 360
D 325 DLPSTAADPVEKSKYKNAEAKDYFLGMFLYEAARRHPHYFAPPELLFFAKRYKAAFTCCQADKAACLLP 384
QY 361 CAAADPHECYAKVDFEFKPLVEEPONLJKONCELFPEQOLGEYKFNQALVRYTKKVPQVST 420
D 385 CAEGDPPACVGLVAFQPLVVEEPONLJKONCELFPEQOLGEYKFNQALVRYTKKVPQVST 444
```

262 VHKECCHGDLLECCADRADLAKYICENQDITSTKLKECCDKPILKESHCIASAKRDELPA 321

301 DLPSLAADFVESKDVCKNYAEAKDVFLGMLFYEVARRHPDYVSVLLLRALKTYETTLKCC 360

322 DLNPLEHDFVEDKEVCKNYKEAKDVFLGTFLEYESRRHPDYVSULLRIAKIYEATLDC 381

361 CAAADPHCYAKVDFDEPKLVPEEQNLIKONCELFEOGLGEYKFNALLVRYTKVPQVST 420

382 CAKEDPPACVATVDFKFPQVLDPEQNLIKONCELFEXLGEYGFQNALIVRYTKVPQVST 441

421 PT:VEVSRNLGKVGSKCKHPKAPKMPCAEDYLSWLNOLCVLHEKTPVSDVTKCCTES 480

442 PTUVEVARKUGLVGSRCKKPEERUSCAEDYLSVLRNLCVLHEKTPVSEKVKCCTES 501

481 LVNRRPCFSALEYDETVYPKEFNAETFTFHADICTLSEKERQIKKQATLVELVHKPKAT 540

502 LVNRRPCFSALTPTDITYKPEFVEGTFTFHADLCTLPEDKQIKKQATLVELLKHKPHAT 561

541 KEQLKAMDDFAAFVEKCCXADDKKETCFABEGKLV 576

562 EQQLRTVLGNFAAFVQKCCAAPDHEACFAVEGPKFV 597

RESULT 9

JC5838

albumin - Mongolian jird

C:Species: Meriones unguiculatus (Mongolian jird)

C:Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000

C:Accession: JC5838

R:Yoshida, K.; Seto-Ohshima, A.; Sinohara, H.

DNA Res. 4, 351-354, 1997

A:Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in

A:Reference number: JC5838; MUID:98116663; PMID:9455485

A:Accession: JC5838

A:Molecule type: mRNA

A:Residues: 1-609 <YOS>

A:Cross-references: DDBJ:AB006197; NID:G2317277; PIDN:BAA21765.1; PID:G2317278

A:Experimental source: liver

C:Superfamily: serum albumin; serum albumin repeat homology

F:222-395/Domain: serum albumin repeat homology <SA2>

Query Match 76.9%; Score 2387; DB 2; Length 609;

Best Local Similarity 73.9%; Pred. No. 2,1e-150;

Matches 430; Conservative 65; Mismatches 87; Indels 0; Gaps 0;

QY 2 AHKSEVARRPKDGEENFKALVLIAPQYLOQCQFEDHVKLVNEVTPAKTCVADESAEN 61

DB 27 AHKSEIAHRYKDLGEKYFKGLVLYTFQYLQKCSYEEHVKLVREVTDFASNCADKDESAEN 86

QY 62 CDKSLHTLFGDKLCTVATLRETYGEMADCCAKQSPERNECFLOHKDNPMLPLRVRPVD 121

DB 87 CDKSLHTLFGDKLCSLNFGEKVAEMADCCAKQSPERNECFLOHKDNPMLPPFKRAEPD 146

QY 122 VMCTAFHDNEETFLKKYLYEIAARRHPFYFAPELFFAKRYKAAATECCQAADKAACLTPK 181

DB 147 AMCTAFQENAEAFMGHYLHEVARRHPFYGPPELLYADKYTAVLUTCCCAADCKGACLPK 206

QY 182 LDELDEGKASSAKORUKCASLCKFGGERAFKAWAVARLSQFPKAEFAEVSKLVTLTKV 241

DB 207 LDALKALVSAVRQKLCSSMKFGGERAFKAWAVARMSQFPFNADFAEITKJATDLTKV 266

QY 242 HTECCHGDLLECCADRADLAKYICENQDITSTKLKECCDKPILKESHCIASAEVDEMPAD 301

DB 267 TOECCHGDLLECCADRADLAKYICENQDITSTKLKECCDKPILKESHCIASAEVDEMPAD 326

QY 302 LPSLAADFVESKDVCKNYAEAKDVFLGMLFYEVARRHPDYVSULLLRALKTYETTLKCC 361

DB 327 LPALTADFVEDKVCKNYAEAKDVFLGTFLEYESRRHPDYVSULLLRALKTYEATLDC 386

QY 362 AAADPHCYAKVDFDEPKLVPEEQNLIKONCELFEOGLGEYKFNALLVRYTKVPQVSTP 421

DB 387 AEADPHACYGHVDFDEPKLVPEEQNLIKONCELFEXLGEYGFQNALIVRYTKVPQVSTP 446


```

Db 330 LPSLVKVIEDKEVCKSPAGHDAFMAEFVYVSRHHPDFSIQLIMRIAKGYESLLEKCC 389
QY 362 AAADSEHCYAKVDFEKLPLVEEPQNLKQNCLEFQGLGKYKFNALLVRYTKKVPQVSTP 421
Db 390 KTDNPAECYANAQOLNQHIKETQDVWKNCDLHDHGEADFJKSILIRYTKKVPQVPTD 449
QY 422 TLVEYSRNLGVSKCKKHPKAKMPCAEDYLSVVLNQCVLHKEKTPVSORVTKCCTESL 481
Db 450 LLETKGKQWTTIGTKCCOLGEDRRMACSEGYLSVIHETCRKQETTPINNVSCCQSLY 509
QY 482 VNRPCPSALEVDETVYPKFNATFTTFHADICTLSEKQIKKQKOTALVELVHKPKATK 541
Db 510 ANRRPCFTAMGVDTKYVPPENPOMFSEDEKLCAPAEEREVGQMKLLINLIKRPQWTE 569
QY 542 EQLKAVMDFAAFVEKCKKADKSTCFAEKGLKVAASQAALGL 585
Db 570 EQIKTIADGFTAMVCKQCKQDINTCFEGEGANLIVOSRATLGI 613

RESULT 12
JC4258
alpha-fetoprotein precursor - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 27-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 20-Aug-1999
C:Accession: JC4258
R:Nishio, H.; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczky, A.
Gene 162, 213-220, 1995
A:Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to
A:Reference number: JC4258; MUID:96032345; PMID:7557431
A:Accession: JC4258
A:Molecule type: DNA
A:Residues: 1-609 <NIS>
A:Cross-references: GB:U21916; NID:9841311; PIDN:AAA91641.1; PID:9841312
C:Comment: This protein is a plasma protein produced in the fetal and neonatal liver and
o similar properties and structure.
A:Gene: afp
A:Map position: 3p
A:Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551/
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-609/Product: alpha-fetoprotein #status predicted <MAT>
F:29-202/Domain: serum albumin repeat homology <SAL>
F:221-394/Domain: serum albumin repeat homology <S2>
F:413-592/Domain: serum albumin repeat homology <S3>
F:442,251/Binding site: carbohydrate (Asn; (cova.ent) #status predicted

Query Match 40.4%; Score 1253.5; DB 2; Length 609;
Best Local Similarity 40.1%; Pred. No. 2e-75;
Matches 236; Conservative 115; Mismatches 231; Indels 7; Gaps 3;

QY 3 HKSE-----VAHRFKDLGEENFKALVLAFQYLCQCFEDHVKLVNEVTFATCVADE 57
Db 22 HRNEYGASILDVSOCTAEINLTDLATFFAQPQVQATYKEVSKWVKDALTALBKPGDE 81
QY 58 SAENCDKSLHTLFGDKLCTVATLRTYTGEMADCCAKQEPERNECFLOHKOONP-VLPRLV 116
Db 82 QSAGCLENQLAFLEBELCREKEILEKYGH-SQCCSQSEGRHNCFLAHKPTPASIFFQ 140
QY 117 RPEVVMCTAFHNDDETEKLYEIAIRRHYPFYAPPELLFFAKRYKAAFTCECCQAADKAA 176
Db 141 VPEPTVSCAEYEDRETPMNFVIEIARRHFFLYAPTILLWAARYCKIIPSCCKAENAVE 200
QY 177 CLLPKLDELREGKASSAKQRLKNSLOKQFGERAFKAWAVARLSORPKAEFAVSKLVT 236
Db 201 CFQTKAAATVTKELRESSLNGHACAVMNFGRTFQAIVTKLSQKFTKNFTFIQKLVL 260
QY 237 DLTQVHTCCCHDLLECADRADLAKYICENODSTSSKLECCCKPKLLEKSHCIAEVND 296
Db 261 DVANVHEHCCRGDVLDCLODEKIMSYICSOQDITLSNKITTECKLTTLREGQCIIHEND 320
QY 297 EMPADLPISLAADFVESKDVCKNYAEAKDVFQGMFLYEVARRHPDYVSVVLLLRLLAKTYETT 356

```

RESULT 13

PFHU

```

alpha-fetoprotein precursor [validated] - human
N:Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 08-Dec-2000
C:Accession: A26624; S37655; A93961; A91497; A23699; A61480; A90624; A90757; A93042;
R:Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugaiczky, A.
Biochemistry 26, 1332-1343, 1987
A:Title: Structure, polymorphism, and novel repeated DNA elements revealed by a compl
A:Reference number: A26624; MUID:87185438; PMID:2436661
A:Accession: A26624
A:Molecule type: DNA
A:Residues: 1-609 <GB>
A:Cross-references: GB:M1610; NID:9773678; PIDN:AA585754.1; PID:g178236
R:McVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Krumi
Hum. Mol. Genet. 2, 379-384, 1993
A:Title: A G->A substitution in an HNF I binding site in the human alpha-fetoprotein
A:Reference number: S37655; MUID:93278385; PMID:7684942
A:Accession: S37655
A:Molecule type: DNA
A:Residues: 1-28 <MCV>
A:Cross-references: EMBL:219532; NID:928527; PIDN:CAA79592.1; PID:g28528
A:Note: the authors translated the codon TAT for residue 26 as Thr
R:Morinaga, T.; Sakai, M.; Wegmann, T.G.; Tamaoki, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 4604-4608, 1983
A:Title: Primary structures of human alpha-fetoprotein and its mRNA.
A:Reference number: A93961; MUID:83273664; PMID:6192439
A:Accession: A93961
A:Molecule type: mRNA
A:Residues: 1-609 <WOR>
A:Cross-references: GB:J00077; NID:g311348; PIDN:CAA24758.1; PID:g31351
R:Beattie, W.G.; Dugaiczky, A.
Gene 20, 415-422, 1982
A:Title: Structure and evolution of human alpha-fetoprotein deduced from partial seq
A:Reference number: A91497; MUID:83158778; PMID:6187626
A:Accession: A91497
A:Molecule type: mRNA
A:Residues: 429-556 <BEA>
A:Cross-references: GB:J00076
R:Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.; Teri
Biochemistry 30, 5061-5066, 1991
A:Title: Human alpha-fetoprotein primary structure: a mass spectrometric study.
A:Reference number: A23699; MUID:91242409; PMID:1709810
A:Accession: A23699
A:Molecule type: protein
A:Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
R:Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.
J. Nucl. Med. Allied Sci. 34, 213-216, 1990
A:Title: Characterization of in vitro expressed human alpha-fetoprotein as highly ref
A:Reference number: A61480; MUID:91225826; PMID:1709209
A:Accession: A61480
A:Molecule type: protein

```


[illegible]

```
Db 141 VPEPVTSCEAYESDRETFMKNFIYEIARRHPFLYAPTLILWAARYDKIIPSCCKAENAVE 200
Qy 177 CLLPKLDLDEGKASSAKORLCSASLOKSGERAFKAWAVARLSORPPRAFAEVSCLVT 236
Db 201 CFQTKAATVTKREUSSLLNQHACAVMKNFTGRTFOAITVKLSQKPTKVNFTFIOKLV 260
Qy 237 DLTQVHTCCGGLLECADRADLAKVICENQDSISGKKECCFKLLEKSHCIAEVEND 296
Db 261 DVAHVHCHCCRGVLDCLQDEKATXSYICSQDTLSNKTTECKLTTLERGQCIHAEND 320
Qy 297 EMPADPLSLAADPVESKDVCKNAEAKXDFLGMFLYVYARRHPDYSVVLRLRAXIYETI 356
Db 321 EXPEGLSPNLNRPFLGDRDFNQFSSGKNIPLASFVHEYSRRRPLQAVSVLRVAKGYQEL 380
Qy 357 LKCCAAADPEHCYAKVDFSEKPLVEPQNLIKQNCLEFPLGCEYKFNALLVRYTKVP 416
Db 381 LEKCFQTEPLECQDKEBELQYIQSALAKRSQGLFQKLGYYLQNAFLVAYTKAP 440
Qy 417 QVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC 476
Db 441 QLTSSSELMAITRMATAATCCQLSEDLKACGEAADIIGHLCIRHEMTVPNPGVQC 500
Qy 477 CTSSLVNRPCPSALEVDETVVPKEFNAETFTFHADICTLSEKERQIKKGTALVELVRKH 536
Db 501 CTSSYANRRPCPSLSVDETVVPAPFSDDKFIFHKQLCQAGVALQTMKQEFNLNLVKQK 560
Qy 537 PKATKEOLKAVMDDFAFVKECKKADOKETCPAEFGKLVAAASQAALGL 595
Db 561 PQITEOLETVIADFGSLLEKCCQGGQEGVCFAPBEGOKLSKTRTALGV 609

RESULT 15
ABXL72
74K albumin precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: B41682; S02693; A05288
R:Mockaitis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R.
Mol. Endocrinol. 3, 464-473, 1989
A:Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic acid
during development.
A:Reference number: A41682; MUID:89313788; PMID:2747653
A:Accession: B41682
A:Molecule type: mRNA
A:Residues: 3-607 <MCS>
A:Cross-references: GB:M21442; NID:G213330; PIDN:AAA49637.1; PID:G213331;
R:Schorpp, M.; Doeberling, U.; Wagner, U.; Kyte, G.J.
J. Mol. Biol. 199, 83-93, 1988
A:Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. De-
A:Reference number: S02692; MUID:88172470; PMID:2451026
A:Accession: S02693
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-48 <SCH>
A:Cross-references: EMBL:Z26826
R:Wolfe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, J.L.; Tata, J.
Eur. J. Biochem. 146, 489-496, 1985
A:Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and destabilization
A:Reference number: A05288; MUID:85126974; PMID:3971963
A:Accession: A05288
A:Molecule type: mRNA
A:Residues: 459-502, 'L', 504-557 <WOL>
A:Cross-references: GB:M28276
A:Note: the authors translated the codon TAT for residue 63 as Thr
C:Comment: Serum albumin is synthesized in the liver as prealbumin. It binds copper,
mones (weak bonds with these hormones promote their transfer across the membranes), thy-
C:Genetics:
A:Introns: 27/1
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
F.1-18/Domain: signal sequence #status predicted <Sig>
F.19-24/Domain: propeptide #status predicted <PRO>
```

```
F.25-607/Product: 74K serum albumin #status predicted <MAT>
F.32-201/Domain: serum albumin repeat homology <SA1>
F.220-393/Domain: serum albumin repeat homology <SA2>
F.412-591/Domain: serum albumin repeat homology <SA3>
F.30/Binding site: copper (his) #status predicted
F.80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-3
F.256/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

```
Query Match 38.8%; Score 1205; DB 1; Length 607;
Best Local Similarity 39.3%; Pred. No. 3,3e-72;
Matches 227; Conservative 108; Mismatches 239; Indels 4; Gaps 2;
```

```
Qy 3 HKSEVAHRFKDLGSENFKALVLIATAQVLOQCPDEHVKLNVETEFAKTCAVDESACN 62
Db 30 HKHIAIVYVLTATETPKGLTLA-VSQNLQKSLSELSKLVNEINDFAKSIINDKTPC-C 88
Qy 63 DKSUHTLFGDKLCTVATLRETYGEMADCCAKQEPNERNECFLOHKDDNPNLRVYRVEDV 122
Db 89 EKPVGTLFPDLKADPAVGVNVYWSKECCAKQDPERAQCFKAHRDHEHT---S-KPEPEE 145
Qy 123 MCTAFHDNEETFLKYLVEIARRHPYFYAPELLFPFAKRYKAAFTCCCAADKAACLLPKL 182
Db 146 TKCLXKHPDOLLASFIHEARNHPOLYPAPVALATTKQYHKCAEHCCDEEDKCKCFSEKM 205
Qy 183 DELRDGKASSAKORLKCASLQKFGERAFKAWAVARLSQRPPKAEVSKLVTDLTKVH 242
Db 206 KQLMKQSHSIEDKQHHFCWILDNPFVKVLKALNARVSHRYPEKAEFKLAHNFTEVTHFI 265
Qy 243 TECCHGDLLECDADRADLAKYICENQDSISGKKECCFKLLEKSHCIAEVENDEMPADL 302
Db 266 KDCCHDDMFECMTERLELTHEHTCOHKDELSSKLEKCCNIPLETTYCIYVITLENDDVPAEL 325
Qy 303 PSLAADPVESKDVCKNAEAKXDFLGMFLYVYARRHPDYSVVLRLRAKTYETTLEKCCA 362
Db 326 SQPITEFTEDPHVCEKYAENNEVFLGRYLHVAVRKHQELSEQFLQSAKEVESLNNCKCK 385
Qy 363 AADPHECYAKVDFEKLVEEPQNLIKONCELPQGLYKFNQALLVRYTKVPQVSTPT 422
Db 386 TDNPECYKDGADRPMNEAKERFAYLKQNCIDLHEHGYLFENELLIRYTKKMPQVSDET 445
Qy 423 LVEVSRNLGKVGSKCKKPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTESLV 482
Db 446 LIGIAHQMAD:GEHCACVNPENQRMPCASGDLTILGKMCERQKKTFFKNHVAHCCDTSYS 505
Qy 483 NRRPCFSALEVDVETVVPKEFNAETFTFHADICTLSEKERQKKOTALVELVKHFKPKATKE 542
Db 506 GNRSCFTALGDEDDVYPPVTDITFHPDDKICTANDKEKQHIKQKFLVKLKVSPKLEKN 565
Qy 543 QLKAVMDDFAFVKECKKADOKETCPAEFGKLVAAASQ 580
Db 566 HIDECSABFLKMVQKCCCTADEHQPCFDTKPVZ-EHCQ 603
```

Search completed: October 27, 2003, 15:07:59
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2003, 14:54:42 ; Search time 26 Seconds
(without alignments)
1058.101 Million cell updates/sec

Title: US-09-832-501-18

Perfect score: 3103

Sequence: 1 DAHKSEVAHRFKDLGEBNFK.....TCFAEEGKXIVAAQAALGL 565

Scoring table: ELOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3103	100.0	609	1	ALBU_HUMAN
2	2942	94.8	600	1	ALBU_MACMC
3	2620	84.4	608	1	ALBU_FELCA
4	2562	82.6	608	1	ALBU_CANFA
5	2475.5	79.8	607	1	ALBU_HORSE
6	2450.5	79.0	607	1	ALBU_BOVIN
7	2446	78.8	608	1	ALBU_RABIT
8	2432.5	78.4	607	1	ALBU_SHEEP
9	2426	78.2	608	1	ALBU_RAT
10	2411.5	77.7	605	1	ALBU_PIG
11	2387	76.9	609	1	ALBU_MERUN
12	2378	76.6	608	1	ALBU_MOUSE
13	1557.5	50.2	615	1	ALBU_CHICK
14	1253.5	40.4	609	1	FETA_PANTR
15	1249.5	40.3	609	1	FETA_HUXAN
16	1242.5	40.0	609	1	FETA_GORGO
17	1205	38.8	607	1	FETA_XENLA
18	1200	38.7	609	1	FETA_HORSE
19	1164.5	37.5	606	1	ALBU_XENLA
20	1084	34.9	605	1	ALBU_MOUSE
21	1067	34.4	611	1	FETA_RAT
22	1055	34.0	599	1	AFAM_HUMAN
23	944	30.4	611	1	AFAM_MOUSE
24	928	29.9	608	1	AFAM_RAT
25	747.5	24.1	608	1	ALBU_SALSA
26	742.5	23.9	608	1	ALBU_SALSA
27	699	22.5	382	1	ALBU_RANCA
28	440.5	14.2	1423	1	ALBU_PETMA
29	386	12.4	474	1	VTDB_HUMAN
30	381	12.3	476	1	VTDB_RAT
31	378	12.2	476	1	VTDB_RABIT
32	372	12.0	472	1	VTDB_MOUSE
33	151.5	4.9	1605	1	RRL1_MOUSE

34	144.5	4.7	8797	1	SNB1_HUMAN	Q8nf91, homo sapien
35	138.5	4.5	1410	1	RRL1_HUMAN	Q9p2e9, homo sapien
36	133.5	4.3	1391	1	MST2_DROHY	Q8696, drosophila
37	132.5	4.3	2230	1	GOG4_HUMAN	Q13439, homo sapien
38	129.5	4.2	1972	1	MYHB_HUMAN	P35749, homo sapien
39	129	4.2	3210	1	CENF_HUMAN	P49454, homo sapien
40	128	4.1	1005	1	RA50_METJA	Q58718, methanococc
41	126.5	4.1	1972	1	MYHB_RABIT	P35748, oryctolagus
42	126	4.1	1189	1	SMC2_CHICK	Q90888, gallus gall
43	126	4.1	3259	1	GIAN_HUMAN	Q24789, homo sapien
44	125	4.0	3038	1	TRIO_HUMAN	Q75962, homo sapien
45	124.5	4.0	1790	1	USO1_YEAST	P25386, saccharomyc

ALIGNMENTS

RESULT 1
ALBU_HUMAN
ID ALBU_HUMAN STANDARD; PRT: 609 AA
AC P02768; O95574; Q13140; Q9P157; Q9P177; Q9UHS3; Q9UJZ0;
DT 21-JUL-1986 (Rel. 01, Created)
CT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196112; PubMed=3009475;
RA Minghetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,
RA Beattie W.G., Dugaiczky A.;
RT "Molecular structure of the human albumin gene is revealed by
RT nucleotide sequence within q11-22 of chromosome 4.";
RL J. Biol. Chem. 261:6747-6757(1986).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LYS-420.
RX MEDLINE=82081882; PubMed=6171778;
RA Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
RA Najarian R.C., Seeburg P.H., Wion K.L.;
RT "The sequence of human serum albumin cDNA and its expression in E.
RT coli.";
RL Nucleic Acids Res. 9:6103-6114(1981).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT GLY-121.
RX MEDLINE=82105994; PubMed=6275391;
RA Dugaiczky A., Law S.W., Dennison O.E.;
RT "Nucleotide sequence and the encoded amino acids of human serum
RT albumin mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675).
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
RA Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;
RT "Functional prediction of the coding sequences of 121 new genes
RT deduced by analysis of cDNA clones from human fetal liver.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378.
RA Huang M.C., Wu H.T.;
RT "The cDNA sequences of human serum albumin.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.

- RC TISSUE=Liver, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8].
RP SEQUENCE OF 25-609.
RX MEDLINE=76187907; PubMed=1225573;
RA Meloun B., Moravek L., Kosicka V.;
RT "Complete amino acid sequence of human serum albumin.";
RL FEBS Lett. 58:134-137(1975).
RN [9].
RP SEQUENCE OF 25-609.
RA Brown J.R., Shockley P., Behrens P.Q.;
RL (In) Bing D.H. (eds.);
RL The chemistry and physiology of the human plasma proteins, pp.23-40,
RL Pergamon Press, New York (1979).
RN [10].
RP SEQUENCE OF 1-455 FROM N.A.
RC TISSUE=Liver;
RA Meraya J., Parrilla R., Ayuso M.S.;
RL Submitted (MAR-1995) to the EXBL/GenBank/DBJ databases.
RN [11].
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=86140099; PubMed=2419329;
RA Urano Y., Watanabe K., Sakai M., Tamaoki T.;
RT "The human albumin gene. Characterization of the 5' and 3' flanking
regions and the polymorphic gene transcripts.";
RL J. Biol. Chem. 261:3244-3251(1986).
RN [12].
RP SEQUENCE OF 222-229.
RX MEDLINE=76257808; PubMed=955075;
RA Walker J.E.;
RT "Lysine residue 199 of human serum albumin is modified by
acetylacetic acid.";
RL FEBS Lett. 66:173-175(1976).
RN [13].
RP SEQUENCE OF 25-44 AND 480-499.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [14].
RP DISULFIDE BONDS.
RA Sabar M.A., Stockbauer P., Moravek L., Meloun B.;
RT "Disulfide bonds in human serum albumin.";
RL Collect. Czech. Chem. Commun. 42:564-579(1977).
RN [15].
RP BILIRUBIN-BINDING SITE.
RX MEDLINE=78186630; PubMed=656055;
RA Jacobsen C.;
RT "Lysine residue 240 of human serum albumin is involved in high-
affinity binding of bilirubin.";
RL Biochem. J. 171:453-459(1978).
- RM [16].
RX MEDLINE=87157744; PubMed=3828358;
RA Brennan S.O., Herbert P.;
RT "Albumin Canterbury (313 Lys-->Asn). A point mutation in the second
domain of serum albumin.";
RL Biochim. Biophys. Acta 912:191-197(1987).
RN [17].
RP VARIANTS NAG-2 AND NAG-3.
RX MEDLINE=88068523; PubMed=3479777;
RA Takahashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
RA Satoh C., Neel J.V.;
RT "Amino acid substitutions in inherited albumin variants from
Amerindian and Japanese populations.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
RN [18].
RP VARIANTS NAG-1; HIR-1; HIR-2 AND TOCHIGI.
RX MEDLINE=89345611; PubMed=2762316;
RA Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M.,
RA Neel J.V., Sakurabayashi I., Putnam F.W.;
RT "Point substitutions in Japanese alloalbumins.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
RN [19].
RP VARIANTS MANAJS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
RX MEDLINE=90115905; PubMed=2404284;
RA Arai K., Madison J., Shimizu A., Putnam F.W.;
RT "Point substitutions in albumin genetic variants from Asia.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
RN [20].
RP DESCRIPTION OF VARIANT REDHILL.
RX MEDLINE=90115852; PubMed=2104980;
RA Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
RT "Albumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of
human serum albumin whose precursor has an aberrant signal peptidase
C-cleavage site.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
RN [21].
RP VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTA LYS-106.
RX MEDLINE=91062352; PubMed=2247440;
RA Galliano M., Mirchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
RA Watkins S., Putnam F.W.;
RT "Mutations in genetic variants of human serum albumin found in
Italy.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
RN [22].
RP VARIANTS VENEZIA.
RX MEDLINE=91296740; PubMed=2068071;
RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
RA Mirchiotti L., Putnam F.W.;
RT "A donor splice mutation and a single-base deletion produce two
carboxyl-terminal variants of human serum albumin.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN [23].
RP VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23;
RX KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.
RX MEDLINE=92052189; PubMed=1946412;
RA Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E.,
RA Matsuda Y.-I., Amaki I., Putnam F.W.;
RT "Genetic variants of serum albumin in Americans and Japanese.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
RN [24].
RP VARIANT CASEBROOK ASN-518.
RX MEDLINE=91316157; PubMed=1859851;
RA Peach R.J., Brennan S.O.;
RT "Structural characterization of a glycoprotein variant of human serum
albumin: albumin Casebrook (494 Asp-->Asn).";
RL Biochim. Biophys. Acta 1097:49-54(1991).
RN [25].
RP VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
RX MEDLINE=92190239; PubMed=1347703;
RA Mirchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
RA Rochu D., Porta F.;
RT "Two alloalbumins with identical electrophoretic mobility are produced

Query Match 100.0%; Score 3103; DB 1; Length 603;
 Best Local Similarity 100.0%; Pred. No. 1.7e-194;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVLIAPQYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 Db DAHKSEVAHRFKDLGEENFKALVLIAPQYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 84
 Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDNPNLPLVRPEV 120
 Db NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDNPNLPLVRPEV 144
 Qy 121 DVMTCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 180
 Db DVMTCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 204
 Qy 181 KLDELDEGKASSAKQRLKASLOKQGERAFKAWAVARLSQRPFAEFAEVSKLVTDLTK 240
 Db KLDELDEGKASSAKQRLKASLOKQGERAFKAWAVARLSQRPFAEFAEVSKLVTDLTK 264
 Qy 241 VHTCECHGDLLECCADDRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
 Db VHTCECHGDLLECCADDRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 324
 Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLCMFLYEYARRHPYVSVLLRLAKTYETTLK 360
 Db DLPSLAADFVESKDVCKNYAEAKDVFLCMFLYEYARRHPYVSVLLRLAKTYETTLK 384
 Qy 361 CAADHPCEYAKVDFEKPPLVEEPONLIKONCELFELQGEYKFNALLVRYTKKVPQVST 420
 Db CAADHPCEYAKVDFEKPPLVEEPONLIKONCELFELQGEYKFNALLVRYTKKVPQVST 444
 Qy 421 PTLVEVRNLGKVGSKCKKHPKAEKMPCAEDYLSVNLNOLCVLHEKTPVSDRVTKCCTES 480
 Db PTLVEVRNLGKVGSKCKKHPKAEKMPCAEDYLSVNLNOLCVLHEKTPVSDRVTKCCTES 504
 Qy 481 LVNRRPFCSALEVEDYVVPKEFNATETTFHADICTLSEKERQIKQTALVELVKHKPKAT 540
 Db LVNRRPFCSALEVEDYVVPKEFNATETTFHADICTLSEKERQIKQTALVELVKHKPKAT 564
 Qy 541 KEQLKAVMDDPAAVFEKCKCKADKTCFAEKGKLVAAASQAALG 585
 Db KEQLKAVMDDPAAVFEKCKCKADKTCFAEKGKLVAAASQAALG 609

RESULT 2
 ID ALBU_MACMU STANDARD; PRT; 600 AA.
 AC Q28522;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor (fragment).
 GN ALB.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 CX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93211971; PubMed=8460152;
 RA Watkins S.A., Sakamoto Y., Madison J.M., Davis E.W., Smith D.G.,
 RA Dwulet J., Putnam F.W.;
 RT in bilirubin binding.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2469-2413(1993).
 CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloidal osmotic pressure of blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- ISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch)
 CC
 CC EMBL; M90463; AAA36956.1; --
 DR PIR: A47391; A47391.
 DR HSSP: P02768; 1E7B.
 DR InterPro: IPR000264; Serum_albumin.
 DR Pfam: PF00273; Transport_prot; 3.
 DR PRINTS: PR00802; SERUMALBUMIN.
 DR ProDom: PD002486; Serum_albumin; 1.
 DR SMART: SM00103; ALBUMIN_3.
 DR PROSITE: PS00212; ALBUMIN; 3.
 KW Metal-Binding; Lipid-binding; Repeat; Signal; Copper.
 FT NON_TER 1 1
 FT SIGNAL <1 10 BY SIMILARITY.
 FT PROPEP 11 16 BY SIMILARITY.
 FT CHAIN 17 600 SERUM ALBUMIN.
 FT DOMAIN 17 197 ALBUMIN 1.
 FT DOMAIN 204 389 ALBUMIN 2.
 FT DOMAIN 396 587 ALBUMIN 3.
 FT METAL 19 19 COPPER (BY SIMILARITY).
 FT BINDING 256 256 BILIRUBIN (POTENTIAL).
 FT DISULFID 69 78 BY SIMILARITY.
 FT DISULFID 91 107 BY SIMILARITY.
 FT DISULFID 106 117 BY SIMILARITY.
 FT DISULFID 140 185 BY SIMILARITY.
 FT DISULFID 184 193 BY SIMILARITY.
 FT DISULFID 216 262 BY SIMILARITY.
 FT DISULFID 261 269 BY SIMILARITY.
 FT DISULFID 281 295 BY SIMILARITY.
 FT DISULFID 294 305 BY SIMILARITY.
 FT DISULFID 332 377 BY SIMILARITY.
 FT DISULFID 376 385 BY SIMILARITY.
 FT DISULFID 408 454 BY SIMILARITY.
 FT DISULFID 453 464 BY SIMILARITY.
 FT DISULFID 477 493 BY SIMILARITY.
 FT DISULFID 492 503 BY SIMILARITY.
 FT DISULFID 530 575 BY SIMILARITY.
 FT DISULFID 574 583 BY SIMILARITY.
 SQ SEQUENCE 600 AA; 67880 MW; E45C871A670E740B CRC64;

Query Match 94.8%; Score 2942; DB 1; Length 600;
 Best Local Similarity 93.5%; Pred. No. 4.8e-184;
 Matches 545; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVLIAPQYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 60
 Db DAHKSEVAHRFKDLGEENFKALVLIAPQYLQCCPFEDHVKLVNEVTEFAKTCVADESAAE 76
 Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDNPNLPLVRPEV 120
 Db NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDNDNPNLPLVRPEV 136
 Qy 121 DVMTCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 180
 Db DVMTCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAAACLLP 196
 Qy 181 KLDELDEGKASSAKQRLKASLOKQGERAFKAWAVARLSQRPFAEFAEVSKLVTDLTK 240
 Db KLDELDEGKASSAKQRLKASLOKQGERAFKAWAVARLSQRPFAEFAEVSKLVTDLTK 256
 Qy 241 VHTCECHGDLLECCADDRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 300
 Db VHTCECHGDLLECCADDRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPA 316

Qy 541 KEQLKAVMDDFAAFVEKCKCKADDDKETCFAPGKGLVAASQAAL 583
 ||||| || ||||| ||||| :||| ||||| ||||| :|||
 Db 565 DEQLKTVMGDFGAFVEKCKCAAENKEGCFSEEGPKLVAASQAAL 607

RESULTS

```

RESUL: 5
ALBU_HORSE
ID      ALBU_HORSE      STANDARD;      PR: 607 AA.
AC      P35747;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Serum albumin precursor.
GN      ALB.
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC      NCBI_TaxID=9796;
RN      []]
RP      SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RC      TISSUE=Liver;
RX      MEDLINE=93345495; PubMed=8344282;
RA      Ho J.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;
RT      "X-ray and primary structure of horse serum albumin (Equus caballus)
RT      at 0.27-nm resolution.";
RL      Eur. J. Biochem. 215:305-212(1993).
CC      -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC      binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC      hormones, bilirubin and drugs. Its main function is the regulation
CC      of the colloidal osmotic pressure of blood.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: Plasma.
CC      -1- SIMILARITY: BELONGS TO THE AL5/APP/VDB FAMILY.
CC      -1- SIMILARITY: Contains 3 albumin domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announcement/
CC      or send an email to license@isb-sib.ch).

```

```

CC
ENBL; X74045; CAA52194.1; -.
DR DR
PTR; S34053; ABHOS.
DR DR
HSP; P02768; 1E7B.
DR DR
InterPro: IP000264; Serum_albumin.
DR DR
Pfam; PF00273; transport_prot; 3.
DR DR
PRINTS; PRC08C2; SERUMALBUMIN.
DR DR
ProDom; PD002486; Serum_albumin; 1.
DR DR
SMART; SM00103; ALBUMIN; 3.
DR DR
PROSITE; PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 607
FT DOMAIN 25 204
FT DOMAIN 211 396
FT DOMAIN 403 594
FT METAL 27 27
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 200
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 339 384
FT DISULFID 383 392
FT DISULFID 415 461

```

FT	DISULFID	460	471	
FT	DISULFID	484	500	
FT	DISULFID	499	510	
FT	DISULFID	537	582	
FT	DISULFID	581	590	
SQ	SEQUENCE	607 AA; 68598 MW; 25676E8030A1B90C5 CRC64;		

Query Match
 Best Local Similarity 79.8%; Score 2475.5; DB 1; Length 607;
 Matches 445; Conservative 69; Mismatches 68; Indels 1; Gaps 1;

Qy	1	DAHKSEVAHRFKDILGEENFKALVLIAPQVLOQCPEDHVKLVNVEYTEFAKTCVADESAG	60
Db	25	DTHKSEIARRFNDLGEKHFGKLVLPASQVLOQCPEDHVKLVNVEYTEFAKCAADESAG	84
Qy	61	NCDKSLHTLFQDKLCTVATLRETYGENADCCAKQEPERNECEFLQHKDDNPNPRLVRPEV	120
Db	85	NCDKSLHTLFQDKLCTVATLRTATYBELADCCQEPERNECEFLTHKDDHPNLPKL-KPEP	143
Qy	121	DWVCTAFHDNSETFLKXYLIEIARRHPYFYFAPELLFPAKRYKAAFTTECCQAADKACLLP	180
Db	144	DAQCAAFQEDPKFLGKYLEVARRHYPFYFGPELLFAHEYKADFTTECCPADKKACLLP	203
Qy	181	KLUDELRDGKASSAKORLKCASLQKGERAFKAWAVAR-SQRPKPAFAEVAESKLVTDLTK	240
Db	204	KLDALKERILLSSAKERLKCSSFQNGERAVKANSVARLSQKPPKADFAEVSKIYTDLT	263
Qy	241	VHTECHGDDLJECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA	300
Db	264	VHKECHGDLLECADDRADLAKYICEHQDSISGKLKACCDKQPLLOKSHCIAEVKEDDUPS	323
Qy	301	DLPSLAADPFVSKQVCKQYAEAKQVFGMLFVEYARRHPDYSVVLLRLRLAKTYETTLK	360
Db	324	DLPALAADPAEDKICGKYKQAKQVFGTFLFYSRRHPDYSVSLRLRLAKTYEATLEK	383
Qy	361	CAAADPHCYAKVFDEFKPLVEEPQNIKONCELFQOLGEYKFNQALVRYTKVPQVST	420
Db	384	CAEADPPACYRTVPDQFPLVEEPKSLVKKNCDLFEVGEYDFQNALVRYTKKAPQVST	443
Qy	421	PTLVEVSRNLGKVGSKCKQKHPKAPKMPCAEDYLSVTLNQLCVLHEKTPSDRVTKCCTES	480
Db	444	PTLVIGRITLGVSGRCCKPLPESRLPCSENHLALNRLCVLHEKTPVSEKITKCCDTS	503
Qy	481	LVNRRPCFSALVDEYTVYKPEFNAAETTFHADICTLSEKEROIKKOTALVELVKKHPKAT	540
Db	504	LAERRPCFSALDELGEYVYKPFKAETTFHADICTLPEDEKQIKKQSALAEVLVKKHPKAT	563
Qy	541	KEQLKAVMDMDDFAAFVEKCKCKADDKETCFABEGKKLVAASQAAL	583
Db	564	KFCGLKTVLGNFSAFVAKCCGREDKEACFAEGPKLVASSOLAL	606

RESULT 6

RESULT	ALBU BOVIN	STANDARD;	PRT:	607 AA.
ID	ALBU BOVIN			
AC	P02769; Q02787;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Serum albumin precursor (Allergen Bos d 6).			
GN	ALB.			
OS	Cs taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
OC	Bovidae; Bovinae; Bos.			
OC	NCBI_TaxID=9913;			
RP	[1] _			
RP	SEQUENCE FROM N.A.			
RA	Holowachuk E.W., Stoltenberg J.K., Reed R.G., Peters T. Jr.;			
RL	Submitted (AUG-1991) to the EMBL/genbank/DBJ databases.			
RL	[2]			
RP	SEQUENCE FROM N.A., AND VARIANT THR-214.			
RP	TISSUE=Liver;			
RC				

Db 204 K1ETWREKVLASSARQRLRCAS:QKFGERALKAWSVAR:SQKFPKAEFEVETKLVDTLTK 263
 Qy 241 VHTCECHGDLLEACADRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 300
 Db 264 VHKCECHGDLLEACADRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 323
 Qy 301 DLPSSAADFVESKDVCKNVAEAKDVLGMFLYEVARRHPDYVSVLLRLAKTYETLLEKC 360
 Db 324 NLPPLTADPAEDKDVCKNVAEAKDVLGMFLYEVARRHPDYVSVLLRLAKTYETLLEKC 383
 Qy 361 CAADPHECYAKVDFEFLPVLVEPQNLKONCELFQELGEYKFNALLVRYTKVPQVST 420
 Db 384 CAKDDPHACYSTVDFKLKHLVDEPQNLKONCELFQELGEYKFNALLVRYTKVPQVST 443
 Qy 421 PTLVEVSRNLGKVGSKCKHPEAKMPCADYLSVLNQLCVLHKEKTPVSDRVTKCCTES 480
 Db 444 PTLVEVSRNLGKVGSKCKHPEAKMPCADYLSVLNQLCVLHKEKTPVSDRVTKCCTES 503
 Qy 481 LVNRRPCFSALVEVDYVVPKEFNAETFTFHAD:CTLSEKERQ:KKQTALVELVKKPKAT 540
 Db 504 LVNRRPCFSALVEVDYVVPKEFNAETFTFHAD:CTLSEKERQ:KKQTALVELVKKPKAT 563
 Qy 541 KEQLKAVMDPFAAFVEKCKKADKCTCFABEGKLVAAASQAL 583
 Db 564 BEQLKAVMDPFAAFVEKCKKADKCTCFABEGKLVAAASQAL 606

RESULT 7
 ALBU RABIT
 ID ALBU RABIT STANDARD; PRT; 609 AA.
 AC P49065;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Liver;
 RA Sheffield W.P., Syed S., Schuyler P.D.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
 CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidal osmotic pressure of blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U18344; AAB58347.1; -;
 DR HSSP; P02768; 1E78
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24

FT CHAIN 25 608 SERUM ALBUMIN.
 FT DOMAIN 25 205 ALBUMIN 1.
 FT DOMAIN 212 397 ALBUMIN 2.
 FT DOMAIN 404 595 ALBUMIN 3.
 FT METAL 27 27 COPPER.
 FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 289 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 462 BY SIMILARITY.
 FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.
 FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 SQ SEQUENCE 608 AA; CF5B92647AABF9A2 CRC64;
 Query Match 78.8%; Score 2446; DB i; Length 608;
 Best Local Similarity 74.1%; Pred. No. 8.1e-152;
 Matches 433; Conservative 77; Mismatches 74; Indels 0; Gaps 0;
 Qy 1 DAHKEVAHREKDLGEENFKALVLIAPAOVLOCPREDHVLYNEVTEPAKTCVADESAA 60
 Db 25 EAHKEVAHREKDLGEENFKALVLIAPAOVLOCPREDHVLYNEVTEPAKTCVADESAA 84
 Qy 61 NCKSLHITLFGDKLCTVATLRETYGENADCCAKQEPERNECFLOHKODNPNLRLVRPEV 120
 Db 85 NCKSLHITLFGDKLCTVATLRETYGENADCCAKQEPERNECFLOHKODNPNLRLVRPEV 144
 Qy 121 DVMTAFHNDNETFLKYLVEIARRHPYFYAPPELLFPKRYKAAFTCCCOAAKAAACLLP 180
 Db 145 DVLCKAHDDDEKAPFFGHLYEVARRHPYFYAPPELLFYAAYKAYKAILTECCEADKGACLTP 204
 Qy 181 KLDELDEGKASSAKORLKCASLOKFGERAKAWAVARLSORFPKAEFAVSVLVTDLTK 240
 Db 205 KLDELDEGKASSAKORLKCASLOKFGERAKAWAVARLSORFPKAEFAVSVLVTDLTK 264
 Qy 241 VHTCECHGDLLEACADRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 300
 Db 265 VHKCECHGDLLEACADRADLAKYICENODSISSKLKECEKPLLEKSHCIAEVENDEMPA 324
 Qy 301 DLPSSAADFVESKDVCKNVAEAKDVLGMFLYEVARRHPDYVSVLLRLAKTYETLLEKC 360
 Db 325 GLPAVAEEFVEDKDVCKNVAEAKDVLGMFLYEVARRHPDYVSVLLRLAKTYETLLEKC 384
 Qy 361 CAADPHECYAKVDFEFLPVLVEPQNLKONCELFQELGEYKFNALLVRYTKVPQVST 420
 Db 385 CATDDPHACYSTVDFKLKHLVDEPQNLKONCELFQELGEYKFNALLVRYTKVPQVST 444
 Qy 421 PTLVEVSRNLGKVGSKCKHPEAKMPCADYLSVLNQLCVLHKEKTPVSDRVTKCCTES 480
 Db 445 PTLVEVSRNLGKVGSKCKHPEAKMPCADYLSVLNQLCVLHKEKTPVSDRVTKCCTES 504
 Qy 481 LVNRRPCFSALVEVDYVVPKEFNAETFTFHAD:CTLSEKERQ:KKQTALVELVKKPKAT 540
 Db 505 LVNRRPCFSALVEVDYVVPKEFNAETFTFHAD:CTLSEKERQ:KKQTALVELVKKPKAT 564
 Qy 541 KEQLKAVMDPFAAFVEKCKKADKCTCFABEGKLVAAASQAL 584
 Db 565 NDQLKAVMDPFAAFVEKCKKADKCTCFABEGKLVAAASQAL 608

RESULT 8
 ALBU SHEEP
 ID ALBU SHEEP STANDARD; PRT; 607 AA.
 AC P14639;

CC -- TISSUE SPECIFICITY: Plasma.
 CC -- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -- SIMILARITY: Contains 3 albumin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ011413; CAA09617.1; --
 DR EMBL; M16111; AAA37190.1; --
 DR EMBL; X13060; CAA31458.1; --
 DR EMBL; AK010025; BAB26650.1; --
 DR PIR; A05139; A05139.
 DR HSSP; P02768; 1E7B.
 DR SWISS-2DPAGE; P07724; MOUSE.
 DR MGI; 87991; Albi.
 DR InterPro; IPR000264; Serum albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PRO0802; SERUMALBUMIN.
 DR ProDom; PD02486; Serum albumin; 1.
 DR SMART; SMO0103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24
 FT CHAIN 25 608 SERUM ALBUMIN.
 FT DOMAIN 25 205 ALBUMIN 1.
 FT DOMAIN 212 397 ALBUMIN 2.
 FT DOMAIN 404 595 ALBUMIN 3.
 FT METAL 27 27 COPPER.
 FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 289 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 462 BY SIMILARITY.
 FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.
 FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 FT CONFLICT 27 27 H -> D (IN REF. 5).
 FT CONFLICT 33 33 H -> D (IN REF. 5).
 FT CONFLICT 41 41 Q -> I (IN REF. 5).
 SQ SEQUENCE 608 AA; 68692 MW; 292F7C7BED3A61B4 CRC64;
 Query Match 76.6%; Score 2378; DB 1; Length 608;
 Best Local Similarity 72.4%; Pred. No. 2.1e-147;
 Matches 422; Conservative 80; Mismatches 81; Indels 0; Gaps 0;
 QY 1 DAHKSEVAHFKDGEENFKALVLIATFAQYLOQCFFDHVKLVNVEVTEFAKTCVADESAAE 60
 DB 25 EAHKSEIAHRYNDLGEQFKGLVLIATFASQYLOKQSYDEHAKLVQEVDFDFAKTCVADESAA 84
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDNDNPLRLVEPEV 120
 DB 85 NCDKSLHTLFGDKLCAIPLNRENYGELADCTKOEPERNECFLOHKDNDNPLRPFEPPEA 144
 QY 121 DVMCTAFHDNETFLKLYLYIARRHPHYFAPPELLFFAKRYKAAFTCCQAADKAAACLLP 180
 DB 145 EMATCSFKENPTTFNGHYLHEVARHPHYFAPPELLYVAEQNEILTOCCAEAKESCLTP 204
 QY 181 KLDELURDEGKASSAKQRLKASLQKFGERAPKAWAVARLSQRFPAEFAEVSKLVTDLTK 240

DB 205 KLDGVKALVSSVQRKCKSSMQKFGERAPKAWAVARLSQTFNADFAEITKLTATDITK 264
 QY 241 VHTCECHGDLLECADRADLAKY:CEHQDS::SSKJKECCEKPLEKHGHCIAEVENDEMPA 300
 DB 265 VNKECHGDLLECADRADLAKYKCNENQATISSKLTQCCDKPFLKKAHCLSEVEHDTMPA 324
 QY 321 DIPSIAADPFESKCKYNAEAKOVFLGMFLYEVARRHPDYVSVLLRLAKTYETTLK 360
 DB 325 DLPFAAADFVEDQEVCKRYNAEAKOVFLGTFLYEVARRHPDYVSVLLRLAKKYEATLEK 384
 QY 361 CAAADPHCEYAKVDFEFPKPLVEEPQNLIKOKCELFEOLEGYKFNQALVRYTKVPQVST 420
 DB 385 CAEANPPACYGTVLAEFQPLVEEPKLVNCTDLYKELGEYGFQNALVRYTQKAPQVST 444
 QY 421 PTLVEVSRNLKGVSKCKKHPKAMPQAEYDLSVLNQLCVLHEKTPVSDRVTKCCTES 480
 DB 445 PTLVEAARNLGRVGTCTPLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGS 504
 QY 481 LVNRRPCFSALEVDVETVPKFNATFTFHADICTLSEKERQIKKCTALVELVGHKPKAT 540
 DB 505 LVRRPCFSALEVDVETVPKFNATFTFHADICTLSEKERQIKKCTALVELVGHKPKAT 564
 QY 541 KEQLKAVNDDFAAFVEKCKCKADDKETCFABEGKKLVAASQAAL 583
 DB 565 AEQLATVNDFAQFLDTCCKAADKDTCTESTGPNLVTRCKDAL 607
 RESULT 13
 ALEU CHICK STANDARD; PRT; 615 AA.
 ID ALBU CHICK
 AC P19121;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Casady A.I., Salkild C.K., Baverstock P., Wallace J.C.;
 RJ Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-28 FROM N.A.
 RX MEDLINE=83161037; PubMed=6187737;
 RA Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.;
 RT "The 5' noncoding and flanking regions of the avian very low density
 RT apolipoprotein II and serum albumin genes. Homologies with the egg
 RT white protein genes";
 RL J. Biol. Chem. 258:4556-4564 (1983).
 RN [3]
 RP SEQUENCE OF 19-30.
 RX MEDLINE=78019943; PubMed=911327;
 RA Rosen A.M., Geller D.M.;
 RT "Chicken microsomal albumin: amino terminal sequence of chicken
 RT proalbumin";
 RL Biochem. Biophys. Res. Commun. 78:1060-1066 (1977).
 CC -- FUNCTION: Serum albumin, the main protein of plasma, has a good
 CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidal osmotic pressure of blood.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- TISSUE SPECIFICITY: Plasma.
 CC -- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -- SIMILARITY: Contains 3 albumin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; X60688; CAA43098.1; -;
 CC DR EMBL; V00381; CAA23680.1; -;
 CC DR PIR; S15571; ABCHS;
 CC DR HSP; P02768; IE7B;
 CC DR InterPro; IPR000264; Serum_albumin.
 CC DR Pfam; PF00273; transport_prot; 3.
 CC DR PRINTS; PR00802; SERUMALBUMIN.
 CC DR ProDom; PD002486; Serum_albumin; 1.
 CC DR SMART; SM00103; ALBUMIN_3.
 CC DR PROSITE; PS00212; ALBUMIN; 3. Repeat; Signal; Copper.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18
 FT PROPEP 19 23
 FT CHAIN 24 615 SERUM ALBUMIN.
 FT DOMAIN 24 209 ALBUMIN 1.
 FT DOMAIN 216 401 ALBUMIN 2.
 FT DOMAIN 408 599 ALBUMIN 3.
 FT METAL 30 30 COPPER (BY SIMILARITY).
 FT DISULFID 80 89 BY SIMILARITY.
 FT DISULFID 102 118 BY SIMILARITY.
 FT DISULFID 117 128 BY SIMILARITY.
 FT DISULFID 152 197 BY SIMILARITY.
 FT DISULFID 196 265 BY SIMILARITY.
 FT DISULFID 228 274 BY SIMILARITY.
 FT DISULFID 273 281 BY SIMILARITY.
 FT DISULFID 293 307 BY SIMILARITY.
 FT DISULFID 306 317 BY SIMILARITY.
 FT DISULFID 344 389 BY SIMILARITY.
 FT DISULFID 398 397 BY SIMILARITY.
 FT DISULFID 420 466 BY SIMILARITY.
 FT DISULFID 465 476 BY SIMILARITY.
 FT DISULFID 489 505 BY SIMILARITY.
 FT DISULFID 504 515 BY SIMILARITY.
 FT DISULFID 542 587 BY SIMILARITY.
 FT DISULFID 586 595 BY SIMILARITY.
 FT CARBOHYD 500 500 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 24 24 F -> M (IN REF. 3).
 SQ SEQUENCE 615 AA; 69918 MW; E59E4B5CAEC066C6 CRC64;

Query Match 50.2%; Score 1557.5; DS 1; Length 615;
 Best Local Similarity 46.7%; Pred. No. 4.3e-94;
 Matches 273; Conservative 118; Mismatches 192; Indels 1; Gaps 1;

QY 3 HKSEVAHRFKDLGEENFKALVLAFAQYLOQCFEDHVKLVNEVTEFAKTCVADESAENC 62
 DB 30 HKSEIAHRYNDLKEETFKAVAMITFAQYLQRCSEGLSKLVKDVVDLAQKCVANEDAPEC 89
 QY 63 DKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLPR-LVRPEVD 121
 DB 90 SKPLPSIILDETQCEKLRDSDVGAMADCCSKADPERNECFJSFKVSDPDPQYQRRASD 149
 QY 122 VMCTAFHDNEETFLKKYLYEIAARRIPYFYAPPELLFFAKRYKAAFTCCQAADKAACLPLK 181
 DB 150 VICOEYQDNRVSGFLGHFIYSVARRHFFLYAPAILSPAVDFEHALQSCCKESDVGACLDTK 209
 QY 182 LDELREDEGKASSAKQLKCSLOKGERAFKAWAVARLSQRFPKAPAEVSKLVTLTKV 241
 DB 210 EIVMREKAGVSKVQYVFCGILKQFGDRVFQARQLIYLSOKYPKAPFSEVSKFVHDSIGV 269
 QY 242 HTECHGDLLECCADDPADLAUKYICENQDSISSKLKCECKPILKSHCIATVENDMEMAD 301
 DB 270 HKECEGDMVECCDDMARMMNLCSQQDFVFSKGIKDCCEKPIVERSQCIEMAEAFDEKPAD 329
 QY 302 LPSLAADFVSKDCKVKNYAEAKDVF-GMFLXYARRHPDYSVVLLRLAKTYETTELKCC 361
 DB 330 LPSLVEKYIEDKVCCKSFAGHDADFMAEFVYYSRRHPFESQLIMRIAKGVESLJEXCC 389

QY 362 AAADPHCEYAKVDFDEPKPLVEBPQMLIKONCELFEOLOGYEKFONALLVSYTKVPOVSTP 421
 DB 390 KTDNPAECYANQEQUNQHIKETQDVVTKNCCOLLHGHGEADFLKSLRYTKMPOVPTD 449
 QY 422 TLVVESRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRYTKCCTESL 481
 DB 450 LLLCTGKMTTIGTKCCQLGEDRRMACSGYLSIVIHDTCRKOETTPINDNVSCCSQJY 509
 QY 482 VNERPCFSALEVDETYVPKEFAETTFPHADICTLSEKERQIKKQTALVELYKHKEKATK 541
 DB 510 ANRRPCFTAMGVDTRYVPPFPNPFMFSDFKLCSAPAESEVGGMKLLINLTKRPQMT 569
 QY 542 EQLKAVMDDFAAAFVEKCKKADDKETCFABEGKLVAAASQAALGL 585
 DB 570 EQIKTIADGFTAMVDKCKCKQSDINTCFEGEGANLIVQSRATLGI 613

RESULT 14
 PETA_PANTR ID PETA_PANTR STANDARD; PRT; 609 AA.
 AC Q28789;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-fetoprotein precursor (Alpha-fetog-obulin) (Alpha-1-fetoprotein).
 DE fetoprotein).
 GN AFP.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID:9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96032345; PubMed=7557431;
 RA Nishio H., Gibbs P.E., Minghetti P.P., Zielinski R., Dugaiczky A.;
 RT "The chimpanzee alpha-fetoprotein-encoding gene shows structural
 RT similarity to that of gorilla but distinct differences from that of
 RT human.";
 RL Gene 162:213-220(1995).
 CC -!- FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND
 CC BILIRUBIN LESS WELL THAN, SERUM ALBUMIN. ONLY A SMALL PERCENTAGE
 CC (LESS THAN 2%) OF THE HUMAN AFP SHOWS ESTROGEN-BINDING PROPERTIES.
 CC -!- SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION
 CC TO THE MONOMERIC FORM.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma. Synthesized by the fetal liver and
 CC yolk sac.
 CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; U21916; AAA91641.1; -;
 CC PIR; JC4258; JC4258.
 CC HSP; P02768; IE7B.
 CC DR InterPro; IPR000264; Serum_albumin.
 CC DR Pfam; PF00273; transport_prot; 3.
 CC DR PRINTS; PR00802; SERUMALBUMIN.
 CC DR ProDom; PD002486; Serum_albumin; 1.
 CC DR SMART; SM00103; ALBUMIN_3.
 CC DR PROSITE; PS00212; ALBUMIN; 2.
 KW Glycoprotein; Sulfation; Repeat; Metal-binding; Copper; Nickel;
 KW Signal.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT CHAIN 19 609 ALPHA-FETOPROTEIN.
 FT DOMAIN 20 205 ALBUMIN 1.
 FT DOMAIN 212 397 ALBUMIN 2.


```

FT DOMAIN 404 595 ALBUMIN 3.
FT METAL 22 22 COPPER AND NICKEL (BY SIMILARITY);
FT DISULFID 99 114 BY SIMILARITY.
FT DISULFID 113 124 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. .) (POTENTIAL);
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL);
SQ SEQUENCE 609 AA; 68741 MW; C032987CADCE672B CRC64;

Query Match 40.4%; Score 1253.5; DB 1; Length 609;
Best Local Similarity 40.1%; Pred. No. 2.4e-74;
Matches 236; Conservative 115; Mismatches 231; Indels 7; Gaps 3;

QY 3 HKSE-----VAHRRKDLGEEFNFKALVLIAPAOYLQOCPEFEDHVKLVNEVTEFAKTCVADE 57
DB 22 HNEVGIASILDYSOCTAINEINDLATIFFAQFQVEATYKSEKRVMDALTAIEKPTGDE 81
QY 58 SAENCKSJHTLFGKLCVTATLRETYGEMADCCAKQEPERNECFLOHKDNP-NLPRLV 116
DB 82 OSAGLEQLPAFLBELCREKLEKYGH-SDCCSQSEGRHNCFLAHKKPTPASIFFQ 140
QY 117 REVDMCTAFDNEETLKKVLYBIARRHPYFYAPELLFFAKRYKAAFTCCCAAKAA 176
DB 141 VZPVTSCAEYEDRETFMKNFIYIARRHPFLYAPTILLWAARYDKIIPSCCAENAVE 200
QY 177 CLLPKLDLDRDEGKASSAKQRLKASLOKFGERAFKAWAVARLSORPPKFAFVSKLVT 236
DB 201 CQTAAVTIKELRESSLLNQHACAVKNFGTRTFOA-TVTKLSQKFTKVNFTBIQKLV 260
QY 237 DLTKVHTCCGGDLLECADRADLAKYICENQDISSKLKECKEPLLEKSHCIAEVND 296
DB 261 DVARVHECHCRGVDLQDQGEKIMSYCSQODT-SNKITECKLTTLERQCQIHAEND 320
QY 297 ENPADLPSLADPVESKQVKNYAKQVFLQMGFLMELYEYARRHPDYSVLLRLAKTVETT 356
DB 321 EKPEGLSPNLNFGLDRDFNCFSSGGEKNIFLASFVHEYSRRHPQLAVSVILRVAKGYOEL 380
QY 357 LEKCCAAADPHCYAKVDFEFKPLVVEEPQNLIKQNCSELFQOLGEYKFONALLVRYTKVP 416
DB 381 LEKCFQTEPLECDQKGEELQKYIOESQALAKRSCGJFQKLGELYLQNAFLVATKKAP 440
QY 417 QVSTPTLVEVSNLKGKSKCKHPEAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVTKC 476
DB 441 QLTSELMAITKMAATAATCQLQSEDLLACGEAADIIGHLCIRHETTPVNPVGQC 500
QY 477 CTSELVNRPCPSALEVEDYVPKFFNAETFTFHADICTLSEKEROIKKCTALVELVKHK 536
DB 501 CTSSVANRRPCFSSLVVDYVPPAFSDOKFLFHKDLCCAGVALQTKQBFLLNLVKQK 560
QY 537 PRATKEQLKAVNDDFAAFVEKCKQADDDCTCFABEGKKLVAASCAALGL 585
DB 561 PQITEQLAEVADTSGLLEKCCQGEQEVCFABEGSKLISKTRALGV 609

RESULT 15
FETA HUMAN
ID FETA HUMAN STANDARD; PART; 609 AA.
AC P02771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

```

DE Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
DE fetoprotein).
DE APP.
GN Homo sapiens (Human).
CS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83273664; PubMed=6192439;
RA Morinaga T., Sakai M., Wegmann T.G., Tamaoki T.;
RT "Primary structures of human alpha-fetoprotein and its mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4604-4608(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87185438; PubMed=2436661;
RA Gibbs P.E.M., Zielinski R., Boyd C., Dugaiczky A.;
RT "Structure, polymorphism, and novel repeated DNA elements revealed by
a complete sequence of the human alpha-fetoprotein gene.";
RL Biochemistry 26:1332-1343(1987).
RN [3]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=93278385; PubMed=7684942;
RA McVey J.H., Michaelides K., Hansen L.P., Ferguson-Smith M.,
Tilghman S., Krumlauf R., Tuddenham E.G.D.;
RT "A G->A substitution in an HNF I binding site in the human alpha-
fetoprotein gene is associated with hereditary persistence of alpha-
fetoprotein (HPAFP).";
RL Hum. Mol. Genet. 2:379-379(1993).
RN [4]
RP SEQUENCE OF 429-556 FROM N.A.
RX MEDLINE=83158778; PubMed=6187626;
RA Beattie W.G., Dugaiczky A.;
RT "Structure and evolution of human alpha-fetoprotein deduced from
partial sequence of cloned cDNA.";
RL Gene 20:415-422(1982).
RN [5]
RP PARTIAL SEQUENCE OF 19-609.
RX MEDLINE=91242409; PubMed=1709810;
RA Pucci P., Siciliano R., Malorni A., Marino G., Tecce M.F.,
Ceccarini C., Terrana B.;
RT "Human alpha-fetoprotein primary structure: a mass spectrometric
study.";
RL Biochemistry 30:5061-5066(1991).
RN [6]
RP PRELIMINARY SEQUENCE OF 19-35.
RX MEDLINE=77242506; PubMed=70228;
RA Yachnin S., Hsu R., Heinrikson R.L., Miller J.B.;
RT "Studies on human alpha-fetoprotein. Isolation and characterization
of monomeric and polymeric forms and amino-terminal sequence
analysis.";
RL Biochim. Biophys. Acta 493:418-428(1977).
RN [7]
RP PRELIMINARY SEQUENCE OF 19-38.
RX MEDLINE=78001760; PubMed=711198;
RA Aoyagi Y., Ikenaka T., Ichida F.;
RT "Comparative chemical structures of human alpha-fetoproteins from
fetal serum and from ascites fluid of a patient with hepatoma.";
RL Cancer Res. 37:3663-3667(1977).
RN [8]
RP PRELIMINARY SEQUENCE OF 19-39.
RX MEDLINE=75018719; PubMed=4138095;
RA Ruoslahti E., Pihko H., Vaheri A., Seppala M., Virolainen M.,
Kontinen A.;
RT "Alpha fetoprotein: structure and expression in man and inbred mouse
strains under normal conditions and liver injury.";
RL Johns Hopkins Med. J. Suppl. 3:249-255(1974).
RN [9]
RP GENE STRUCTURE
RX MEDLINE=85182629; PubMed=2580830;
RA Sakai M., Morinaga T., Urano Y., Watanabe K., Wegmann T.G.,
Tamaoki T.;
RT "The human alpha-fetoprotein gene. Sequence organization and the 5'

```

Search completed: October 27, 2003, 15:05:17
Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2003, 15:01:33 ; Search time 105 Seconds
(without alignments)
1437.722 Million cell updates/sec

Title: US-09-832-501-18
Perfect score: 3103
Sequence: 1 DAHKSEVAHFQDLGEENFK.....TCFAEESGKLVAASQAALGL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 259052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2504	80.7	608	5 Q95VB7	Q95vb7 schistosoma
2	2374	76.5	608	11 Q8C7H3	Q8c7h3 mus musculu
3	2336	75.3	576	11 Q8C7C7	Q8c7c7 mus musculu
4	1865.5	60.1	396	4 Q8IUK7	Q8iuk7 homo sapien
5	1295.5	41.7	527	13 Q8JIA9	Q8jia9 sphendonod p
6	1242	40.0	609	6 Q8MJU5	Q8mju5 canis famil*
7	1242	40.0	626	13 Q8UW05	Q8uw05 ambystoma m
8	1218.5	39.3	610	6 Q8MJ76	Q8mj76 sus scrofa
9	1087	35.0	624	13 Q8UW06	Q8uw06 ambystoma t
10	1082	34.9	605	11 Q8BK65	Q8bk65 mus musculu
11	1076	34.7	605	11 Q8BK56	Q8bk56 mus musculu
12	1045	33.7	400	13 Q8JIA7	Q8jia7 sphendonod p
13	955	30.8	603	13 Q8YGH6	Q8ygh6 rana shqipe
14	928.5	29.9	614	13 Q8J134	Q8j134 naja naja (
15	888	28.6	406	13 Q8J1A8	Q8j1a8 hoplodactyl
16	739	23.8	205	11 Q8C7J4	Q8c7j4 mus musculu

17	723	23.0	417	11 Q8ROJ9	Q8roj9 mus musculu
18	376.5	12.1	484	13 Q9W6F5	Q9w6f5 gallus gall
19	373	12.0	476	11 Q9CY31	Q9cy31 mus musculu
20	372	12.0	476	11 Q9IXG1	Q9ixg1 mus musculu
21	365	11.8	551	13 Q42279	Q42279 petromyzon
22	331	10.7	122	13 Q90WZ8	Q90wz8 larus argen
23	290	9.3	123	13 Q90WZ6	Q90wz6 poephila gu
24	264	8.5	135	11 Q63205	Q63205 rattus norv
25	188	6.1	1723	2 Q9JMX8	Q9jmx8 helicobacte
26	184	5.9	1819	16 Q9ZLV0	Q9zlv0 helicobacte
27	184	5.9	1927	16 Q25262	Q25262 helicobacte
28	162.5	5.2	44	6 Q95MC2	Q95mc2 equus cabal
29	162.5	5.2	680	5 Q9V6S8	Q9v6s8 drosophila
30	161	5.2	1079	3 Q96V11	Q96v11 pneumocysti
31	156	5.0	1026	3 Q74669	Q74669 pneumocysti
32	154.5	5.0	3843	5 Q9USD0	Q9usd0 drosophila
33	153.5	4.9	661	5 Q8MS79	Q8ms79 drosophila
34	153.5	4.9	3843	5 Q9VU94	Q9v94 drosophila
35	153	4.9	62	6 Q8M1L1	Q8m1l1 sus scrofa
36	150	4.8	1065	3 Q01828	Q01828 pneumocysti
37	149	4.8	40	6 Q9TRAS	Q9tra5 cryptotagus
38	148	4.8	1028	3 Q74668	Q74668 pneumocysti
39	144.5	4.7	8749	4 Q8NF91	Q8nf91 homo sapien
40	142.5	4.6	2755	10 Q9LJ70	Q9lj70 arabidopsis
41	141.5	4.6	1560	5 Q26644	Q26644 strongyloce
42	138.5	4.5	1069	3 Q96V12	Q96v12 pneumocysti
43	137.5	4.4	1348	16 Q8YK55	Q8yk55 anabaena sp
44	135.5	4.4	2841	5 Q8MLU9	Q8mlu9 drosophila
45	135.5	4.4	2931	5 Q9W2C6	Q9w2c6 drosophila

ALIGNMENTS

RESULT 1

ID	Q95VB7	PRELIMINARY;	PRT;	608 AA.
AC	Q95VB7			
DT	01-DEC-2001 (TREMblrel. 19, Created)			
DT	01-DEC-2001 (TREMblrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMblrel. 23, Last annotation update)			
DE	Albumin.			
OS	Schistosoma mansoni (Blood fluke).			
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;			
OC	Schistosomatoidea; Schistosomatidae; Schistosoma.			
OX	NCBI_TaxID=6183;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;			
RT	"Albumin precursor homolog is a novel T helper cell immunogenic egg			
RT	component in murine infection with Schistosoma mansoni.";			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF418550; AAL08579.1;			
DR	InterPro; IPR000264; Serum_albumin.			
DR	Pfam; PF00273; transport_prot; 3.			
DR	ProTIS; PRO0802; SERUMALBUMIN.			
DR	ProDom; PD002486; Serum_albumin; 1.			
DR	SMART; SM00103; ALBUMIN; 3.			
DR	PROSITE; PS00212; ALBUMIN; 2.			
SC	SEQUENCE 608 AA; 68225 MW; E5EABB28E1C66B54 CRC64;			
Query Match	80.7%;	Score 2504;	DB 5;	Length 608;
Best Local Similarity	76.3%;	Pred. No. 1.7e-188;		
Matches 445;	Conservative 79;	Mismatches 59;	Indels 0;	Gaps 0;

Qy	1	DAHKSEVAHFQDLGEENFKALVIAFAOVLQCPEDHVKLVNEVTEFAKTCVADESSE 60
Db	25	DAHKSEIAHFQDLGEQHFGLVIAFSPQLQCPVEEHVKLVNEVTEFAKTCVADESSE 84
Qy	61	NCDKSLHTLFDKLCVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVRPEV 120
Db	85	NCDKSLHTLFDKLCVATLRLSDSYGELADCCAKOEPERNECFLOHKDDHNPFPVRPDA 144

```
QY 122 DVMCTAFHNEBTFUKKYLVEIARRHPYFAPPELLFFPAKRYKAAPTECCQAAQKAACLJP 180
DB 145 EAMCTSFQENAVTFMGHLYHEVARRRHPYFAPPELLYYAEKYSALMTECCGADKAACITP 204
QY 181 KLDELDECKASSAKORLKCASLQKFGGERAFKAWAVARLSORFPKAEFAEVS KLVTDLTK 240
DB 205 KLDAUKKALASSVNRLLKCSLQRFQORAFKAWAVARLSQFPKADFAEITKLA-DLTK 264
QY 241 WHITECHGDLLECCADRADLAKYICENODSISSKLEKCEKPLLEKSHCIAEVENDMPA 300
DB 265 LTBEECHGDLLECCADRAELAKYMCENASISSKLOACCDPVLKXSHCLSEVENDLPA 324
QY 301 DLPSLAAAFVESKOVCKNYAEAKDVLGMFLVEYARRHPDYSDVSVLLLR LAKYTETLEK 360
DB 325 DLPSLAAAFVEDEKCKNYAEAKDVLGMFLVEYARRHPDYSDVSVLLLR LAKYKYEATLEK 384
QY 361 CAADAPHECYAKVDFEFPKPLVEEPONLIKONCELFQOLGEYKFNALLVRYTKVPOVST 420
DB 385 CAADAPSCYGVKLVDFEFPKPLVEEPONLIKONCELFQOLGEYKFNALLVRYTKVPOVST 444
QY 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEAARNLGVKSGCKCVLPQAORLPCVEDYISAILNRVCVLHEKTPVSEHVTKCCSGS 504
QY 481 LVNRRPCFSALVDETYVPKFEPAETFTPHADICTLSEKERQIKKOTALVELVKKHPKAT 540
DB 505 VVRRPCFSALVDETYVPKFEPAETFTPHADICTLSEKERQIKKOTALVELVKKHPKAT 564
QY 541 KEOLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAAL 583
DB 565 GQOLATVLGEGTAFADJCKCKAEDKEACFSEDGPKLVASSQAAL 607
```

```
RESULT 2
Q8C7H3 PRELIMINARY; PRT; 608 AA.
ID Q8C7H3
AC Q8C7H3
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Albumin 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK050248; BAC34145.1; -.
SQ SEQUENCE 608 AA; 68722 MW; 292F60EEDD3A61B4 CRC64;
```

```
Query Match 76.5%; Score 2374; DB 11; Length 608;
Best Local Similarity 72.2%; Pred. No. 2.7e-178;
Matches 421; Conservative 80; Mismatches 82; Indels 0; Gaps 0;

QY 1 DAHSEVARRFKDLGEENFKALVIAFAQYLOQCFEDHVKLVNEVTEFAKTCVADESAAE 60
DB 25 EAHKSEIARHYNDJGQHFHGLVLIAFSQYLQKCSYDEHAKLVQEVTFDAKTCVADESAA 84
QY 61 NCDKSLHTLFGKLCVTATLRETYGEMADCCAKQBPNERNECFLOHKDNDPNLRLVRREV 120
DB 85 NCDKSLHTLFGKLCVPAIPLNRENYGELADCCCTKQBPNERNECFLOHKDNDPNLPPRPEA 144
QY 121 DVMCTAFHNEBTFUKKYLVEIARRHPYFAPPELLFFPAKRYKAAPTECCQAAQKAACLJP 180
DB 145 EAMCTSFQENAVTFMGHLYHEVARRRHPYFAPPELLYYAEKYSALMTECCGADKAACITP 204
```

```
QY 181 KLDELDECKASSAKORLKCASLQKFGGERAFKAWAVARLSORFPKAEFAEVS KLVTDLTK 240
DB 205 KLDAUKKALASSVNRLLKCSLQRFQORAFKAWAVARLSQFPKADFAEITKLA-DLTK 264
QY 241 WHITECHGDLLECCADRADLAKYICENODSISSKLEKCEKPLLEKSHCIAEVENDMPA 300
DB 265 VNBEECHGDLLECCADRAELAKYMCENQATISSKLOTCDDKPLLKXSHCLSEVENDTMPA 324
QY 301 DLPSLAAAFVESKOVCKNYAEAKDVLGMFLVEYARRHPDYSDVSVLLLR LAKYTETLEK 360
DB 325 DLPALAAAFVEDEKCKNYAEAKDVLGMFLVEYARRHPDYSDVSVLLLR LAKYKYEATLEK 384
QY 361 CAADAPHECYAKVDFEFPKPLVEEPONLIKONCELFQOLGEYKFNALLVRYTKVPOVST 420
DB 385 CAEAPPACVGTVLAEFQPLVEEPKLVKTNCDLVEKLGEGYGFONAILVRYTKVPOVST 444
QY 421 PTLVEVSRNLGVKSGCKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DB 445 PTLVEAARNLGRVGTCKCTLPEORLPCVEDYLSAILNRVCVLHEKTPVSEHVTKCCSGS 504
QY 481 LVNRRPCFSALVDETYVPKFEPAETFTPHADICTLSEKERQIKKOTALVELVKKHPKAT 540
DB 505 LVERRPCFSALTVDYTYVPKFEPAETFTPHADICTLPEKEKQIKKOTALAEVKKHPKAT 564
QY 541 KEOLKAVMDDDFAAFVEKCKKADDKETCFABEGKKLVAASQAAL 583
DB 565 AEQLKTMDDFAFLDTCCKAADKDTCTFSTEGPNLVTRCKDTL 607
```

```
RESULT 3
Q8C7C7 PRELIMINARY; PRT; 576 AA.
ID Q8C7C7
AC Q8C7C7
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Albumin 1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK050644; BAC34360.1; -.
FT NON_TER
SQ SEQUENCE 576 AA; 65002 MW; F85733E99AE37F04 CRC64;
```

```
Query Match 75.3%; Score 2336; DB 11; Length 576;
Best Local Similarity 72.2%; Pred. No. 2.5e-175;
Matches 415; Conservative 79; Mismatches 81; Indels 0; Gaps 0;

QY 9 HRFKDLGEENFKALVIAFAQYLOQCFEDHVKLVNEVTEFAKTCVADESAAE 68
DB 1 NRYNDLGEQHFHGLVLIAFSQYLQKCSYDEHAKLVQEVTFDAKTCVADESAAE 60
QY 69 LFGDKLCVTATLRETYGEMADCCAKQBPNERNECFLOHKDNDPNLRLVRREVDMCTAFH 128
DB 61 LFGDKLCVPAIPLNRENYGELADCCCTKQBPNERNECFLOHKDNDPNLPPRPEAEAMCTSF 120
QY 129 DNEBTFUKKYLVEIARRHPYFAPPELLFFPAKRYKAAPTECCQAAQKAACLJPKLDELDE 188
DB 121 ENPTTFMGHLYHEVARRRHPYFAPPELLYYAEQYNEILTQCCAEADKESCLTLPKLDGK 180
QY 189 GKASSAKORLKCASLQKFGGERAFKAWAVARLSORFPKAEFAEVS KLVTDLTKVHTECHG 248
DB 181 ALVSSVRQRMCKSSMQKFGGERAFKAWAVARLSOTFPNADFAEITKLA-DLTKVHTECHG 240
```

QY 249 DLLECADDRADLAKYICENODSISSKLKECCBPLLEKSHCIAEVENDEMPADPLSLAAD 308
 DB 241 DLLECADDRADLAKYICENODSISSKLKECCBPLLEKSHCIAEVENDEMPADPLSLAAD 300
 QY 309 FVSEKDVCKNYAEAKDVLGMLFELYEYARRHPDYSVLLLRKAKTYETTLKCCAAADPHE 368
 DB 301 FVEDQEVCKNYAEAKDVLGMLFELYEYARRHPDYSVLLLRKAKTYETTLKCCAAADPHE 360
 QY 369 CYAKVDFEFKPLVEEPONLIKONCELFQELGEYKFNALLVRYTKKVPQVSTPTLVEVSR 428
 DB 361 CYGTVLAEFQPLVEEPONLIKONCELFQELGEYKFNALLVRYTKKVPQVSTPTLVEVSR 420
 QY 429 NLGKVGKCCCKHPKAPKMPCAEDYLSVNLQCVLHEKTPVSDRVTKCTTESLVNRRPCF 488
 DB 421 NLGRVGTCKCTPLPDQRLPCVEDYLSAIVNRVCLJHEKTPVSHVTKCCSGSLVRRPCF 480
 QY 489 SALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKPKATKEQLKAVM 548
 DB 481 SALTVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKPKATKEQLKAVM 540
 QY 549 DDFAAVFEKCKADDDKTCFAEEGKKLVAASQAAL 583
 DB 541 DDFAAVFEKCKADDDKTCFAEEGKKLVAASQAAL 575
 RESULT 4
 Q81UK7 ID Q81UK7 PRELIMINARY; PRT; 396 AA.
 AC Q81UK7;
 DT 01-MAR-2003 (TremBLrel. 23, Created)
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
 DE Similar to serum albumin precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBC databases.
 DR EMBL; BC035969; AAH35969.1;
 SQ SEQUENCE 396 AA; 45159 MW; 756519C096463A9B CRC64;

Query Match 60.1%; Score 1865.5; DB 4; Length 396;
 Best Local Similarity 63.6%; Pred. No. 1.6e-138;
 Matches 372; Conservative 0; Mismatches 0; Indels 213; Gaps 1;
 QY 1 DAHSEVAHREKDLGEENFKALVLAFAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAE 60
 DB 25 DAHSEVAHREKDLGEENFKALVLAFAQYLQOCPPFEDHVKLVNEVTEFAKTCVADESAE 84
 QY 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPRPEV 120
 DB 85 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPRPEV 144
 QY 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 DB 145 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 153
 QY 181 KLDELRLDECKGASSAKORLKASQKFGFRAPKAWAVARLSORFPKAEFAEVSKLVTLTK 240
 DB 164 ----- 163
 QY 241 VITECCHGDLLECADDRADLAKYICENODSISSKLKECCBPLLEKSHCIAEVENDEMPA 300
 DB 164 ----- 163
 QY 301 DLPSLAADPVESKDVCKNYAEAKDVLGMLFELYEYARRHPDYSVLLLRKAKTYETTLK 360
 DB 164 ----- 171

QY 361 CAADAPHECYAKVDFEFKPLVEEPONLIKONCELFQELGEYKFNALLVRYTKKVPQVST 420
 DB 172 CAADAPHECYAKVDFEFKPLVEEPONLIKONCELFQELGEYKFNALLVRYTKKVPQVST 23;
 QY 421 PTLVEVSRNLGKVGKCCCKHPKAPKMPCAEDYLSVNLQCVLHEKTPVSDRVTKCTTES 480
 DB 232 PTLVEVSRNLGKVGKCCCKHPKAPKMPCAEDYLSVNLQCVLHEKTPVSDRVTKCTTES 291
 QY 481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKPKAT 540
 DB 292 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKEROIKKOTALVELVKKPKAT 35;
 QY 541 KEQLKAVMDDFAAVFEKCKADDDKTCFAEEGKKLVAASQAALGL 585
 DB 352 KEQLKAVMDDFAAVFEKCKADDDKTCFAEEGKKLVAASQAALGL 396
 RESULT 5
 Q8JIA9 ID Q8JIA9 PRELIMINARY; PRT; 527 AA.
 AC Q8JIA9;
 DT 01-OCT-2002 (TremBLrel. 22, Created)
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
 DE Serum albumin (Fragment).
 OS Sphenodon punctatus (Hatteria) (Tuatara).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
 OX NCBI_TaxID=8508;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Metcalf V.J.; Brennan S.O.; George P.M.; Charbets G.K.;
 RT "Partial coding sequence for Sphenodon punctatus 68 kDa albumin."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBC databases.
 DR EMBL; AF375971; AA046104.1;
 DR InterPro; IPR000264; Serum albumin.
 DR Pfam; PF00273; transport prot.; 3.
 DR PRINTS; PR00802; SSRUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 FT NON TER 1
 SQ SEQUENCE 527 AA; 59711 MW; C62B799E387F5929 CRC64;

Query Match 41.7%; Score 1295.5; DB 13; Length 527;
 Best Local Similarity 45.9%; Pred. No. 1.4e-93;
 Matches 240; Conservative 92; Mismatches 188; Indels 3; Gaps 3;
 QY 62 CDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPRPEV 120
 DB 5 CDKSLHTLFGDKLCTVATLRETYGEMADCCAKOEPERNECFLOHKDDNPNLRLVPRPEV 63
 QY 121 DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPPELLFFAKRYKAAFTCCQAADKAACLLP 180
 DB 64 EVSKLYODDLTLGNYIYEVARHPYLVQVPPVFATASLYDEALTKCCQADAKATCFHP 123
 QY 181 KLDELRLDECKGASSAKORLKASQKFGFRAPKAWAVARLSORFPKAEFAEVSKLVTLTK 240
 DB 124 RIPPLIEVLKMSNGIQENTCGILKKFGERTLKATKLVQMSQKPKADPATINKLVEDITH 183
 QY 241 VITECCHGDLLECADDRADLAKYICENODSISSKLKECCBPLLEKSHCIAEVENDEMPA 300
 DB 184 MHTECCRGDTLLECLRDREALTEVTCSHKDAISSKLPTCCCEKSVLREGCEVRLVENDOKPA 243
 QY 301 DLPSLAADPVESKDVCKNYAEAKDVLGMLFELYEYARRHPDYSVLLLRKAKTYETTLK 360
 DB 244 DLSEIAEYIIPDHVCHOHLAKBOAFKAKFLYEVSRHPPELSTLGLVGVKGVQELLERC 303
 QY 361 CAADAPHECYAKVDFEFKPLVEEPONLIKONCELFQELGEYKFNALLVRYTKKVPQVST 420
 DB 304 CKTDNPPCYQAADLKKHIAQFQELVQNCNLYNTLGGYLFHALLIRYTKRMPQLTS 363

```
QY 421 PTLVEVSRNLGKVGSKCKHPEAKRMPKCAEDYLSVLNCLCVLHEKTPVSDRVTKCTTES 480
Db 364 BELFYTR-ITKAASRCCEVSVDKLPCTSYGVDFVLGGICQHRQSSINNVNQCSCNS 422
QY 481 LVNRRPCFSALEVDYVXPKEFNAETFTFHAD:CTLSEKERQIKKQTAALVELVYKHKPKAT 540
Db 423 YALRSLCITS:GGDEKFPVIEFSADLFTFHEDLCHAACDKLQERKQMIYNLVYKHKPNIT 482
QY 541 KEQLKAVMDOPAAFEVKKCADDKETCPAEKGLVAASQAAL 583
Db 483 KEQLQTVFGFTQMTKXCCKAEDHEACFGSEKGLVAESQAL 525

RESULT 6
Q8MJU5 PRELIMINARY; PRT: 609 AA.
AC Q8MJU5;
DT 01-OCT-2002 (TremBrel. 22, Created)
DT 01-OCT-2002 (TremBrel. 22, Last sequence update)
DE Alpha-fetoprotein.
GN AFP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Furuichi M., Neo S., Hiasue M., Tsuchiya R., Watanabe M.,
RA Hashizaki K., Hisamatsu S., Yamada T.;
RT "Canine alpha-fetoprotein cDNA."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB089789; BAC07513.1; -
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PRO0802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN_3.
DR PROSITE; PS00212; ALBUMIN_3.
SQ SEQUENCE 609 AA; 68782 MW; B54B0250C5AF2AF0 CRC64;

Query Match 40.0%; Score 1242; DB 6; Length 609;
Best Local Similarity 40.5%; Pred. No. 2.7e-89;
Matches 231; Conservative 113; Mismatches 225; Indels 2; Gaps 2;

QY 16 BENFKALVLIAPAOYLQCCPEDEHVKLVNEVTEFAKTCVADSEAKDKS:HTLFGDKLC 75
Db 40 EMLNVLDTATIFPAQVQATYKSVKMKDILTVEKSTGSEQGGCJENQLFAFLEIC 99

QY 76 TVATLRETYGMAQCCAKQEPERNECEFLQHKD-DNPMLPRLVRPEVDVMCTAFHDNEET 134
Db 100 HEKEISEKYG-LAOCSSQREERHNCFLAHKKAAPPSPFPQVAEPVTSCKAYEENEDMF 158

QY 135 LKKYLVEIARHPYPAPELLFPKRYKAAATECCQAADKAACLLPKLDELREGKASSA 194
Db 159 MNRVYEIARHPYPAETILSLAHYKGIIPLCCKAENAVECFTQTSITLITKELRESSL 218

QY 195 XQRLKASLQKQGERAPKAWAVARLSORFPKAEVSKLVDLTQVHTECHCDLLECA 254
Db 219 LNQHICAVNRNFGPTFPAITVTKLSQKFSKANTEIQKLVLDVAHIEBCCRNVLECL 278

QY 255 DDADLAKYICENQSISSKKECEKPLLEKSHCIAEVENDEMPADLPISLAADFVESKD 314
Db 279 QDGEKIMSVICSQQDILSSKIDACCKLPILGQCIIHAENDGKPEGLSPNLNRFLEERD 338

QY 315 VCQNTAEAKDVLGMFLVEYARRHPDYSVLLLRKATYETITLKKCAAADPHCYAKVF 374
Db 339 FNQFSREKDLFMARFTVEYSRRHTKLAVPVVLAVKGYQELLEKCSQSENPCEQKGE 398

QY 375 DEFKPLVEEPNLIKQCELEQGEYKFNALLVRVTKYPOVSTPTPLVEVSENLCVG 434
Db 399 BELEXYIOESQALRSCGLFQKUGYYLQNAFLVATYTKAQPQLTPPELMAFTRMATAA 458
```

```
QY 435 SKCKCHPEAKRMPKCAEDYLSVLNCLCVLHEKTPVSDRVTKCTTESLVNRR3CFSALEVD 494
Db 459 ATCCQLSDRQIACGEGAADLIIGQLCIRHEETPINPOVGQCCSSSYANRRPCFSSLVVD 518
QY 495 ETVVPKEFNAETFTFHAD:CTLSEKERQIKKQTAALVELVYKHKPKATKEQLKAVMDFAAF 554
Db 519 ETVYIPSPFSADKFIHKLQDLCQAQGVALTQMKQQLINLVKQKPO:TEEQLEAVIADFSL 578
QY 555 VEKCKCADDKETCPAEKGLVAASQAALGL 585
Db 579 LEKCCQGEQEAQCEPEEGPKLISKTRALGV 609

RESULT 7
Q8UM05 PRELIMINARY; PRT: 626 AA.
AC Q8UM05;
DT 01-MAR-2002 (TremBrel. 20, Created)
DT 01-MAR-2002 (TremBrel. 20, Last sequence update)
DE Serum albumin precursor.
GN AaB.
OS Ambystoma maculatum (spotted salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OC NCBI_TaxID=43114;
RN [1]
RP SEQUENCE FROM N.A.
RA TissueLiver;
RA Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.;
RT "Serum albumin of the mole salamanders Ambystoma maculatum and
RT Ambystoma texanum."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217183; AAL56646.1; -
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PRO0802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN_3.
DR PROSITE; PS00212; ALBUMIN_3.
DR SIGNAL.
KW SIGNAL.
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 626 SERUM ALBUMIN.
SQ SEQUENCE 626 AA; 70677 MW; 9D66F57F174AC23F CRC64;

Query Match 40.0%; Score 1242; DB 13; Length 626;
Best Local Similarity 40.1%; Pred. No. 2.8e-89;
Matches 237; Conservative 110; Mismatches 238; Indels 6; Gaps 3;

QY 1 DAHKSEVAHRFKDL---GEENFKALVLIAPAOYLQCCPEDEHVKLVNEVTEFAKTCVAD 56
Db 28 EGVNDVPHLIGDLIPMGVDNSKGVLAAYSQMLPLCPYEEHLQVRVEDVMQIALCAKG 87

QY 57 ESAENCDKSLHTLFQDKLCTVATLRETYGEMADCAKQEPERNECEFLQHKDN-PNLRL 115
Db 88 ARHANCAKSPMTIILDELCKPENAEKYPFHQCECKEDPERHKCFVEHKQANHEELTKY 147

QY 116 VPPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFVAPPELLFPKRYKAAFTCCQAADKA 175
Db 148 VRPAPEIQCKQHAENRGPELLARYIIPMLAIGHPHMTIPAILGFAQRFDGIVSHCCKDVEIA 207

QY 176 A-CLLAPKLDELDEGKASSAKQRLKASLQKQGERAPKAWAVARLSORFPKAEVSKL 234
Db 208 GQCFNDKPKPEHKQEVYVYCALQKHCNYILQDKERALTYAKVAQASOKFPLASFENVQII 267

QY 235 VTDLTKVHTCECHGDLLECCADRADLAKYICENQSISSKKECEKPLLEKSHCIAEVE 294
Db 268 VPDVHLHQTCGGDMWACMLERMKLTAKICEKDELATHLKECCDKPLLEKSACIIRLP 327

QY 295 NDEMPADLPISLAADFVESKDVCKNVAEKADVPLGMFLVEYARRHPDYSVLLLRKATY 354
Db 328 NDQKPADLSPKVPHYIDDPVECKLYTEGDTFMGRFLYECARRHODYSPMLLRMGSGYE 387
```

```
QY 355 TTLEKCCAAADPHCEYAKVDFEFPKPLVEBPQNLIKONCELFQOLGEYKFKQNALLVRYTKK 414
Db 388 EPLKKCCAAEGHNECLAATESLKKIESSVTLTKNCGALDKLKSYLEFQNLIIKPYVAR 447
QY 415 VPOVSTPTLTVESNRNKGKVGSKCKHPEAKRMPCADYLSVNLQCVLHKEKTPVSDRVT 474
Db 448 MPALSEQSLRIITKMTTIGEKCHRPEDQOMTCSGGLGVFGQICMKQKTPVNEKVA 507
QY 475 KCTESLVNRRPCFSALEVDVTVVPKFEFNAETFTPHADICTLSEKEROIKKOTALVELVK 534
Db 508 QCCSHLSQTPCFSALPVDVETTVPPPLSVASFNFDLCTTISEPQQSKKQVFJRLMK 567
QY 535 HKPKATKEQLKAVMDFAAFVEKCCCKADOKETCFABEGKKLVAASQAALGL 585
Db 568 QYEHMTDEQLKTCVNVFPMVDQCCCKADNHNECFALGAKLIDACKAILAV 618

RESULT 8
Q8MJ76 PRELIMINARY; PRT; 610 AA.
AC Q8MJ76;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Serum albumin precursor.
OS Alpha-fetoprotein.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RA Kim J.G., Nonneman D., Vallet J.L., Christenson R.K.;
RT "Mapping of the porcine alpha-fetoprotein (AFP) gene to SSC8.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF517770; AAM66710.1; -.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 2.
SQ SEQUENCE 610 AA; 68624 MW; C985BEAD44963D5E CRC64;

Query Match 39.3%; Score 1218.5; DB 6; Length 610;
Best Local Similarity 39.7%; Pred. No. 1.9e-87;
Matches 227; Conservative 117; Mismatches 225; Indels 3; Gaps 3;

QY 16 BENFKALVLIAPQYLOQCPFDHVKLVNEVTEFAKTCVADESANCKDSLHTLFGDKLC 75
Db 40 EBNVLDLATIFFPAQFVOEATYKEVQNMVDVLTVEKSTGSEQPACCLNQSVFLKEIC 99
QY 76 TVATLRETGEMADCCAKOEPEERNECFLOHKODNP-NLPRLVRPEVDVMTAFHNEET 134
Db 100 HEEIPEIKYG-LSHCCSQSGEEHNCFLARKKAAPASIPFPQVPEVTSCKAYEENRELF 158
QY 135 LKKYLYEIAARRHPFYFAPELLFPFAKYKAAFTBCCQAADKAACLLPKLDELDRDEGKASSA 194
Db 159 MRYEYIEIARRHPFLVAPILSLAAQYDKIIPCCKAENAVECFQTKAASITKEIRESSL 218
QY 195 KQRLKASLOKGERAFKAWAVARLSQRPFAFVSKLVTLTKVHTECHGDLLECA 254
Db 219 LNQHMTCTVMROFCARTFRAITVTKLSQKFPKANFTSIQKLV-LVAHIHEECCRGVLECL 278
QY 255 DQADLAKYICENQDSISKLKCECKBP-LLEKSHCIAEVENDENPADLPSSLAADFVSK 313
Db 279 QDAERVSVYVCSQDDTLSSKIAECCKLPTTLLELQGCIHAENDDKPEGLSPNLNRFGLGR 338
QY 314 DVCKYABAKDVLGMLFLEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHCEYAKV 373
Db 339 DFNQLSSREKDLSMARTYYSRRHKKLAVPVLVAKGYQELLEKCSOSENPLECQDKG 398
QY 374 DFEFKPLVEBPQNLIKONCELFQOLGEYAKFQNALLVRYTKKPVQVSTPTLTVESNRNKGK 433
```

```
Db 399 EEELEKYIOESQALAKRSCGLFQKLGVEYVLQNALVAVTKKAPOLTPPELMALTRKMATT 458
QY 434 GSKCKCKHPEAKRMPCADYLSVNLQCVLHKEKTPVSDRVTKCTESLVNRRPCFSALEV 493
Db 459 GAAACHJESQDLQACGGAADLIIGOLCIIRHEEPINPVGVCCTSSYANRRPCFSSLLV 518
QY 494 DETVVPKFEFNAETFTPHADICTLSEKEROIKKOTALVELVKHKPKATKEQLKAVMDFAA 553
Db 519 DETVVPKFEFNAETFTPHADICTLSEKEROIKKOTALVELVKHKPKATKEQLKAVMDFAA 578
QY 554 FVEKCCCKADOKETCFABEGKKLVAASQAALGL 585
Db 579 LLEKCCQCEQEVCFABEGPALISKTRASLGV 610

RESULT 9
Q8UWJ6 PRELIMINARY; PRT; 624 AA.
AC Q8UWJ6;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Serum albumin precursor.
OS Ambystoma texanum (Smallmouth salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomataidae;
OC Ambystoma.
OX NCBI_TaxID=8104;
RN [1]
SEQUENCE FROM N.A.
RA Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B.;
RT "Serum albumin of the mole salamanders Ambystoma maculatum and
RT Ambystoma texanum.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217182; AAL56645.1; -.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 624 AA; 70321 MW; DE08533BF4953EF7 CRC64;

Query Match 35.0%; Score 1087; DB 13; Length 624;
Best Local Similarity 37.7%; Pred. No. 4.3e-77;
Matches 214; Conservative 102; Mismatches 240; Indels 12; Gaps 5;

QY 14 LGENFKALVLIAPQYLOQCPFDHVKLVNEVTEFAKTCVADESANCKDSLHTLFGDK 73
Db 45 IGVEHAKALAMALFSQMSLCKPHEHQVQVRVNVMDIADLCRGAHGDCGKSVVITLNE 104
QY 74 LCTVATLRETGEMADCCAKOEPEERNECFLOHKODNP-NLPRLVRPEVDVMTAFHNEE 132
Db 105 LCKTPENPEKYPFHGCKCKDEDPERHKCF-EHKSTDPKERTYEVYKPSFQICKQHAENRD 164
QY 133 TFLKKYLYEIAARRHPFYFAPELLFPFAKYKAAFTBCCQAADKAACLLPKLDELDRDEGKA 191
Db 165 EFLGHYIHKVASSHTTMYPPALLSFTLHFDGIVSHCKCKDEATVGCCLSEKMPAKHEVEH 224
QY 192 SSAYQRLKASLOKGERAFKAWAVARLSQRPFAFVSKLVTLTKVHTECHGDL 251
Db 225 VCAVQKNCNYTLQNFNERALRASKAHACSKFPHASFENVQRLTDGIVHLHOTCGGDM 284
QY 252 ECADDRADLAKYICENQDSISKLKCECKBP-LLEKSHCIAEVENDENPADLPSSLAADFVE 311
Db 285 ACMAERMKLITQTCEK-----KKCEKPVLSERSEIVLPLNDEKPADLSPEVRYFD 336
QY 312 SKVCKKNYAEAKDVLGMLFLEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHCEYAK 371
```

```

Db      337 DPEVCKRPEKGDAPYGRFLCOYAKIPEHSAENLRIASGLEKAYKTCAGAHNECIA 336
QY      372 KVDFEFKPLVEEPQNLIKONCELFQGLGEYKFQNALLVRYTKVPQVSTPTLVEVSNL 431
Db      397 KEEETLRHEIEASKTKLTTCGALKGLPGYHFQINIMIVRYTGILPRSSDAFLVYTKLT 456
QY      432 KUGSCCKHPKAMPKPCADYLSVVLNQLCVLHEKTPV-SDRVTKCTESLVRRCFSA 490
Db      457 NIGQCKKLPDQQPCSEGGVGYFAQIC-QNQTTFENEXLAHCKDLSFT-PCFAA 515
QY      491 LEVDETYVPKEFNAETFTFHADICTLSEKERQIKKCTALVELVHKPKATKEQLKAYMDC 550
Db      516 LTJVDETYVPAVTAESFNENEFCTPSEADLQAKKQFLMHLVTRHPKIDQVKTS-SEK 575
QY      551 PAAVFEKCKKADDEKTCFAESEGKLVAA 578
Db      576 FLAMGQCKKADQRCNECPATEGAKLVEA 603

RESULT 10
Q8BK65 PRELIMINARY; PRT; 605 AA.
AC Q8BK65;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Alpha-fetoprotein precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK076053; BAC36150.1; -.
SQ SEQUENCE 605 AA; 67322 MW; 049B7A4A8B01E4B CRC64;

Query Match 34.9%; Score 1082; DB 11; Length 605;
Best Local Similarity 35.7%; Pred. No. 1e-76;
Matches 204; Conservative 120; Mismatches 241; Indels 6; Gaps 3;

QY 16 BENFALVLIAPAQYLQCCPFEDHVKLNEVTEFAKTCVADESACNCKSLHTLFGDKLC 75
Db 40 EKNVLSIATITFTQVPEATEEE---VNKMTSDVLAAMKNSGDDGLESQ-SVFLDEIC 95
QY 76 TVATLREYGEVADCCAKQEPERNECFLOHKDDNP-NLPRLVRPEVDVWCTAFHNEET 134
Db 96 HETELSNKYG-LSGCCSGVGRHOCLLARKKTAPASVPPFPFEPAPSCAKAHEENRAVP 154
QY 135 LKKYLYETARRHPYFAPPELLFAKRYKAAFTCCQAAKCAACLPKLDELDEGKASSA 194
Db 155 MNRFIVEVSRNPFMYAPAILSLAAQYDKVVLACCADNKECFQTKRASAKELREGSM 214
QY 195 KORLKCASLOKGEGERAFKAWAVARLSQRPKAPAEVSKLVDLTLYVTECHGDLLECA 254
Db 215 LNEHVCVIRKFGSRNLQATTIKLSQKLTEANFTEIOKLALDVALIHERCCQGSLECL 274
QY 255 DORADLAKYICENODSISSKLKECEKPLEKSHCIAEVENDEMPADLPSLAADFVESKD 314
Db 275 QDGEKVMYICSQQNLISKIAECCKLPMIQLGFCIIHAENGVRPEGLSNPSQFLGDRN 334
QY 315 VCKNYAEAKDVFLGMFLVEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVF 374
Db 335 FAQFSSEKIMFMAGFLHEYSRTHPNLPVSVILRIAKTYQEIILEKCSQSGNLPGCCDNLE 394
QY 372 DEFKPLVEEPQNLIKONCELFQGLGEYKFQNALLVRYTKVPQVSTPTLVEVSNLKG 434
Db 397 KEEETLRHEIEASKTKLTTCGALKGLPGYHFQINIMIVRYTGILPRSSDAFLVYTKLT 456
QY 375 DEFKPLVEEPQNLIKONCELFQGLGEYKFQNALLVRYTKVPQVSTPTLVEVSNLKG 434

```

```

Db      395 EELQKHIEESQALSQSCALYQTLGDYKQLQNLFLIGYTRKAPQLTSELIDLTGMWSIA 454
QY      435 SKCKHPKAMPKPCADYLSVVLNQLCVLHEKTPVSDRVTKCTESLVRRCFSALEVC 494
Db      455 STCCQLSEBKSGGCGEGNADIFIGHLCIRNEASPVNSGISHCCNSSYSNRRLC-TSFLRD 514
QY      495 ERYVPEKFNAEFTTFHADICTLSEKERQIKKCTALVELVHKPKATKEQLKAYMDCFAAF 554
Db      515 EYIAPPPFSEDKPIPHKOLCQAHKALQTMKQELINLVKORPELTBOJAAVTADFSGL 574
QY      555 VEKCKKADDEKTCFAESEGKLVAAASQAALGL 585
Db      575 LEKCKCAQOQEVCFTEEGPKLISKTRDALGV 605

RESULT 11
Q8BK56 PRELIMINARY; PRT; 605 AA.
AC Q8BK56;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Alpha-fetoprotein precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Placenta, and Extraembryonic tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK076197; BAC36249.1; -.
SQ SEQUENCE 605 AA; 67409 MW; CF3509A9EC146110 CRC64;

Query Match 34.7%; Score 1076; DB 11; Length 605;
Best Local Similarity 35.6%; Pred. No. 3.1e-76;
Matches 203; Conservative 120; Mismatches 242; Indels 6; Gaps 3;

QY 16 BENFALVLIAPAQYLQCCPFEDHVKLNEVTEFAKTCVADESACNCKSLHTLFGDKLC 75
Db 40 EKNVLSIATITFTQVPEATEEE---VNKMTSDVLAAMKNSGDDGLESQ-SVFLDEIC 95
QY 76 TVATLREYGEVADCCAKQEPERNECFLOHKDDNP-NLPRLVRPEVDVWCTAFHNEET 134
Db 96 HETELSNKYG-LSGCCSGVGRHOCLLARKKTAPASVPPFPFEPAPSCAKAHEENRAVP 154
QY 135 LKKYLYETARRHPYFAPPELLFAKRYKAAFTCCQAAKCAACLPKLDELDEGKASSA 194
Db 155 MNRFIVEVSRNPFMYAPAILSLAAQYDKVVLACCADNKECFQTKRASAKELREGSM 214
QY 195 KORLKCASLOKGEGERAFKAWAVARLSQRPKAPAEVSKLVDLTLYVTECHGDLLECA 254
Db 215 LNEHVCVIRKFGSRNLQATTIKLSQKLTEANFTEIOKLALDVALIHERCCQGSLECL 274
QY 255 DORADLAKYICENODSISSKLKECEKPLEKSHCIAEVENDEMPADLPSLAADFVESKD 314
Db 275 QDGEKVMYICSQQNLISKIAECCKLPMIQLGFCIIHAENGVRPEGLSNPSQFLGDRN 334
QY 315 VCKNYAEAKDVFLGMFLVEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVF 374
Db 335 FAQFSSEKIMFMAGFLHEYSRTHPNLPVSVILRIAKTYQEIILEKCSQSGNLPGCCDNLE 394
QY 375 DEFKPLVEEPQNLIKONCELFQGLGEYKFQNALLVRYTKVPQVSTPTLVEVSNLKG 434
Db 395 EELQKHIEESQALSQSCALYQTLGDYKQLQNLFLIGYTRKAPQLTSELIDLTGMWSIA 454
QY      435 SKCKHPKAMPKPCADYLSVVLNQLCVLHEKTPVSDRVTKCTESLVRRCFSALEVC 494

```



```
Db 455 STCCOLSEKWCSCGEGMADIFIGHLCIRNEASPVNSG:SHCCNSYSNRRUCIT-SFLRD 514
Qy 495 ETVVPEKFNATFTTHADICTLSEKERO:KKQTALVELVKKHPKATKQOLKAVNDPFAAF 554
Db 515 EYIAPPPSEDFIFHKDUCQACGKALQMKQELLINLVKQPELVEOLAATVADFSL 574
Qy 555 VEKCKADDKETCFABEGKGLVAASQAALGL 585
Db 575 LEKCKCAQDOEVCFTTEGPKL-SKTRDALGV 605

RESULT 12
Q8JIA7
ID Q8JIA7 PRELIMINARY; PRT; 400 AA.
AC Q8JIA7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE A/B over-sized serum albumin (Fragment).
OS Sphenodon punctatus (Hatteria) (Tuatara).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
OX NCBI_TaxID=8508;
RN [1]
SEQUENCE FROM N.A.
RA Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;
RA "Partial mRNA sequence for tuatara A/B serum albumin.";
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375973; AAM461C6.1; -.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 2.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 2.
DR PROSITE; PS00212; ALBUMIN; 2.
FT NON_TER 1
SQ SEQUENCE 400 AA; 45715 MW; 8DB20609657CF753 CRC64;

Query Match 33.7%; Score 1045; DB 13; Length 400;
Best Local Similarity 47.7%; Pred. No. 5,1e-74;
Matches 186; Conservative 80; Mismatches 124; Indels 0; Gaps 0;

Qy 196 QRLKASLCKFGGERAFKAWARLSORFPKAEVSKLVTLTKVHTCCGHDLECAD 255
Db 3 EKHSCGFLASFGGERAFQANKLVLSQKFFKAPFEIHKVVLTKLQKCCGHWIECD 62
Qy 256 DRADLAKYICENQDSISSKLKSCCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV 315
Db 63 DRVEVMAYICSKAVFSSIKDCCEKPIVDREVCIQAOLDEKPADLPISAGCYESTEV 122
Qy 316 CKNYAEAKDVFLGMFLVEYARHDPYSVLLRLAKTYETTLKCCAAADPECYAKVFD 375
Db 123 KXHYEGKGVFLAHFVYVSRHDPFSSQMLRTGKYODTLDKCKTENPECYGKAGE 182
Qy 376 EFKPLVEEPQNLIKONCELFQEGYKFNQALLVRYTKKVPQVSTPTLVEVSRNLGKVG 435
Db 183 ELARHIQESQELKTHCSFYTSQKQPPFKQVLYRYTKOMPQLPAELLIEISKLLTGCV 242
Qy 436 KCKHIPEAKRMPCAEDYLSVNLQCLVJHEKTPVSDRVTKCTTESLVNRRPFCFSALEVD 495
Db 243 KCCPLSEDKRLSCSEKLSMWLFECIROEASPVNNHVTTCDSYSEMRPCTKLGVD 302
Qy 496 TVVPKFNATFTTHADICTLSEKROIKKQTALVELVKKHPKATKQOLKAVNDPFAAF 555
Db 303 SYVPPEFCFSTFLDQCLTAPEEARLKQTLFLVKLIQLKFPQIEQELKLVTDYHAME 362
Qy 556 EKCKADDKETCFABEGKGLVAASQAALGL 585
Db 363 EKCCQAKENQECFSTEGEKLQEGKALLGV 392

RESULT 13
```

```
Q9YGH6
ID Q9YGH6 PRELIMINARY; PRT; 603 AA.
AC Q9YGH6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Serum albumin precursor (Fragment).
GN ALB.
OS Rana shqiperica.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=44326;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Bushat; TISSUE=Liver;
RA Uzzell T., Hotz H.;
RT "Albumin cDNA sequence of Rana shqiperica: evolutionary changes in frog albumins.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U0452; AAD09358.1; -.
DR HSSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Signal.
KW NON_TER 1
FT SIGNAL <1 23
FT CHAIN 24 603
FT SEQUENCE 603 AA; 69293 MW; 340D3723FA010C99 CRC64;

Query Match 30.8%; Score 955; DB 13; Length 603;
Best Local Similarity 33.6%; Pred. No. 9,9e-67;
Matches 190; Conservative 119; Mismatches 241; Indels 16; Gaps 3;

Qy 12 KDLGEENFKALVLIAPQYLQCCFFEDHVKLVNEVTEFAKTCVADESAENCKSLHTLFG 71
Db 37 KAVGKPAVEKLVLMVAQDFEKCSDLEHLKVQAKIIKAVNCEKHPKAECKKPAIELYH 96
Qy 72 DKLCVTATLRETYGEMADCCAKQEPERNECFLOHKDDNPMLPLVR-----PEVDVMCT 125
Db 97 DIVCKEEDIDQLYPTWTECCGKABERTKCFYEHRE-----VRVEYKIPNIESCK 148
Qy 126 AFHNESTFLKYLIEIARHPYFYAPELLFFAKRYKAAATECCQADKAACLPKLDEL 185
Db 149 EKHEHPORAFSYLLNSIAKHSKLYPPAVLGFATQYNEITTECCAAEDKAKCFGERMPQV 208
Qy 186 RDEGKASSAKORLKASLQKFGGERAFKAWARLSORFPKAEVSKLVTLTKVHTEC 245
Db 209 KLTNYLEDKHKQKCVLKEPPEVRSQALTIVQVSQRFGNKYDDVEKVTIEIAHLNEDC 268
Qy 246 CHGDLLECADRADLAKYICENQDSISSKLKSCCEKPLEKSHCIAEVENDEMPADLP 305
Db 269 CKGDAVECMTERMEATEHICLAKELSKLSDCCKAGVLERTPCILALPNEE--PDLPIE 326
Qy 306 AADFVESKDVCKNYAEAKDVFLGMFLVEYARHDPYSVLLRLAKTYETTLKCCAAAD 365
Db 327 LKEYEYDEHVCENYQKQKRYLAHFTHDYSRSHOESSPQSLRVSRGFEMLEKCCASAN 386
Qy 366 PHECYAKVDFBPKPLVEEPQNLIKONCELFQEGYKFNQALLVRYTKKVPQVSTPTLVE 425
Db 387 SAELCKDAPKLELAANKENEEISKQNGCALEKLGFDNFYIQLLVRYGKMPQVTAQLVE 446
Qy 426 VSRNLGKVGSKCKHPKAEKRMPCAEYLSVNLQCLVJHEKTPVSDRVTKCTTESLVNRR 485
Db 447 LTGRMAKIGVYCCGLPDNKKQPCAEKLDILLGEMCEREKKTPIINDNVHCCVDSYANRR 506
Qy 486 PCFSALEVDETYVPKFNATFTTHADICTLSEKROIKKQTALVELVKKHPKATKQOLK 545
Db 507 PCFTKLGPYANYEAPVWDESKLHFTADMKCGSADDQLKTKLVLLVLEFLKMKPTCGEKL 566
```


Qy 532 LVKHKPKATKEQLKAVMDDFAAFEVKCKADDKETCFAPBEGKKLVAASQAAL 583

Dd 354 VVCKPAPITHEQLKAVIDFVGWVEKCHGHNHACFLAGBPQLVORTQAAL 405

Search completed: October 27, 2003, 15:07:11
Job time : 110 secs